

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:30:47 ; Search time 110.427 Seconds

(without alignments)
2295.451 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSLAPSGEGSDRT.....LFAKGEVQNWAI SDHQGRN 495

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495	100.0	495	1	S175 SHEEP
2	61	12.3	495	1	S175 HUMAN
3	32	6.5	495	1	S175 MOUSE
4	12	2.4	363	2	QBWS1
5	12	2.4	436	1	NPT3 HUMAN
6	12	2.4	447	2	QBVCX8
7	12	2.4	466	2	Q8GLH1
8	12	2.4	470	2	Q7YTZ7
9	12	2.4	559	2	Q9VIG7
10	11	2.2	582	2	Q9P2U8
11	11	2.2	582	2	Q920B7
12	11	2.2	582	2	Q8BLE7
13	11	2.2	582	2	Q9J112
14	10	2.0	390	2	Q921B2
15	10	2.0	465	1	NFT1 MOUSE
16	10	2.0	465	1	NFT1 RAT
17	10	2.0	465	2	Q8K3H3
18	10	2.0	465	2	Q91WV5
19	10	2.0	465	2	Q8AZ46
20	10	2.0	476	2	Q9Q579
21	10	2.0	497	2	Q6NR28
22	10	2.0	497	2	Q7KRJ1
23	10	2.0	502	2	Q9VDM0
24	10	2.0	544	1	VRT3 CAEBL
25	10	2.0	544	2	Q7Q580
26	10	2.0	573	2	Q99932
27	9	1.8	69	2	Q91Y99
28	9	1.8	127	2	Q71118
29	9	1.8	395	2	Q65502
30	9	1.8	469	2	Q8CJH8
31	9	1.8	475	2	Q8AZ69

32	9	1.8	479	2	Q23514	caenorhabdi
33	9	1.8	497	2	Q8MRP7	O8mrp7 drosophila
34	9	1.8	498	2	Q8CJH9	Q8cjh9 rattus norv
35	8	1.6	119	2	Q6EX40	Q6ex40 pimelia rad
36	8	1.6	126	2	Q9LRG3	Q9lrg3 chlorella v
37	8	1.6	130	2	Q20936	O20936 simulium vi
38	8	1.6	130	2	Q9T9F5	Q9tf95 hermatobate
39	8	1.6	131	2	Q9TH57	Q9th57 littorina s
40	8	1.6	133	2	Q9XPB9	Q9xpb9 triatoma pr
41	8	1.6	133	2	Q9XPC8	Q9xpc8 rhodnius pr
42	8	1.6	133	2	Q9XPC9	Q9xpc9 rhodnius ro
43	8	1.6	135	2	Q9ZXN3	Q9zxn3 anopheles f
44	8	1.6	136	2	Q94TM4	Q94tm4 cicindela c
45	8	1.6	136	2	Q9G7H1	Q9g7h1 anopheles n
46	8	1.6	136	2	Q9G7H5	Q9g7h5 uranotaenia
47	8	1.6	136	2	Q9G7H6	Q9g7h6 anopheles c
48	8	1.6	136	2	Q9G7H7	Q9g7h7 anopheles s
49	8	1.6	136	2	Q9G7H8	Q9g7h8 chagasia ba
50	8	1.6	136	2	Q9G7H9	Q9g7h9 anopheles a
51	8	1.6	136	2	Q9G7I0	Q9g7i0 anopheles a
52	8	1.6	136	2	Q9G7I1	Q9g7i1 biranella g
53	8	1.6	136	2	Q9G7I2	Q9g7i2 anopheles b
54	8	1.6	136	2	Q9G7I3	Q9g7i3 anopheles c
55	8	1.6	138	2	Q8UE72	Q8ue72 agrobacteri
56	8	1.6	139	2	Q9XKI8	Q9xki8 nezata viri
57	8	1.6	141	2	Q51581	Q51581 plectonema
58	8	1.6	144	2	Q6VTI1	Q6vti1 lygus gemel
59	8	1.6	159	2	Q7YH75	Q7yjh75 spnaerodact
60	8	1.6	160	2	Q21745	Q21745 littorina s
61	8	1.6	160	2	Q79238	Q79238 littorina s
62	8	1.6	160	2	Q79239	Q79239 littorina p
63	8	1.6	160	2	Q99830	Q99830 littorina s
64	8	1.6	160	2	Q34932	Q34932 littorina s
65	8	1.6	160	2	Q9T337	Q9t337 littorina s
66	8	1.6	160	2	Q9T356	Q9t356 littorina s
67	8	1.6	160	2	Q9T3N7	Q9t3n7 littorina p
68	8	1.6	160	2	Q9T3Q3	Q9t3q3 littorina p
69	8	1.6	160	2	Q9T5E2	Q9t5e2 littorina s
70	8	1.6	160	2	Q9T5F0	Q9t5f0 littorina p
71	8	1.6	160	2	Q9T5F1	Q9t5f1 littorina s
72	8	1.6	160	2	Q9T5F2	Q9t5f2 littorina s
73	8	1.6	160	2	Q9T5F3	Q9t5f3 littorina s
74	8	1.6	172	2	Q7PWK3	Q7pwk3 anopheles g
75	8	1.6	178	2	Q9T3K8	Q9t3k8 littorina a
76	8	1.6	178	2	Q9T3K9	Q9t3k9 littorina s
77	8	1.6	178	2	Q9T461	Q9t461 littorina f
78	8	1.6	178	2	Q9THC1	Q9thc1 littorina l
79	8	1.6	178	2	Q9THC2	Q9thc2 littorina l
80	8	1.6	178	2	Q9THC3	Q9thc3 littorina o
81	8	1.6	186	2	Q7YAE8	Q7yae8 thalassoma
82	8	1.6	189	2	Q8HBE4	Q8hbe4 littorina l
83	8	1.6	189	2	Q8HBN7	Q8hbn7 littorina l
84	8	1.6	193	2	Q6DTN7	Q6dtn7 drosophila
85	8	1.6	193	2	Q6DTN8	Q6dtn8 drosophila
86	8	1.6	193	2	Q6DTN9	Q6dtn9 drosophila
87	8	1.6	193	2	Q6DTP0	Q6dtp0 drosophila
88	8	1.6	193	2	Q6DTP5	Q6dtp5 drosophila
89	8	1.6	193	2	Q6DTQ6	Q6dtq6 drosophila
90	8	1.6	193	2	Q6DTQ8	Q6dtq8 drosophila
91	8	1.6	205	2	Q6QTE2	Q6qte2 bolitogloss
92	8	1.6	206	2	Q6QTD0	Q6qtd0 bolitogloss
93	8	1.6	208	2	Q6QTD3	Q6qtd3 bolitogloss
94	8	1.6	211	2	Q9ZZU2	Q9zzu2 littorina s
95	8	1.6	221	2	Q8M7R2	Q8m7r2 rhodnius ro
96	8	1.6	221	2	Q8M7R3	Q8m7r3 rhodnius ro
97	8	1.6	221	2	Q8M7R4	Q8m7r4 rhodnius ro
98	8	1.6	221	2	Q8M7R5	Q8m7r5 rhodnius ro
99	8	1.6	221	2	Q8M7R6	Q8m7r6 rhodnius pr
100	8	1.6	223	2	Q34402	Q34402 euproctus a
101	8	1.6	223	2	Q34860	Q34860 littorina a
102	8	1.6	223	2	Q34861	Q34861 littorina b
103	8	1.6	223	2	Q34867	Q34867 littorina b
104	8	1.6	223	2	Q34871	Q34871 littorina c

105	8	1.6	223	2	Q34892	Q34892 littorina h	178	8	1.6	303	2	Q71BT0	Q71bc0 blackburnia
106	8	1.6	223	2	Q34899	Q34899 littorina k	179	8	1.6	308	1	LiVH_SALTY	P30295 salmonella
107	8	1.6	223	2	Q34906	Q34906 littorina l	180	8	1.6	311	2	Q71BR7	Q71br7 blackburnia
108	8	1.6	223	2	Q34908	Q34908 littorina m	181	8	1.6	311	2	Q71BT4	Q71bc4 blackburnia
109	8	1.6	223	2	Q34914	Q34914 littorina o	182	8	1.6	316	2	Q71BS5	Q71bs5 blackburnia
110	8	1.6	223	2	Q34924	Q34924 littorina p	183	8	1.6	316	2	Q71BS7	Q71bs7 blackburnia
111	8	1.6	223	2	Q34933	Q34933 littorina s	184	8	1.6	316	2	Q71BS6	Q71bs6 oryza sativ
112	8	1.6	223	2	Q34934	Q34934 littorina s	185	8	1.6	320	2	Q71BS4	Q71bs4 blackburnia
113	8	1.6	223	2	Q7GG43	Q7gg43 littorina s	186	8	1.6	321	2	Q7F919	Q7f919 oryza sativ
114	8	1.6	226	2	Q9B388	Q9b388 blackburnia	187	8	1.6	326	2	Q9B707	Q9b707 eurycea wat
115	8	1.6	228	2	Q8LV29	Q8lv29 tarentola e	188	8	1.6	327	2	Q71BR1	Q71br1 blackburnia
116	8	1.6	232	2	Q8M376	Q8m376 austrochilus	189	8	1.6	327	2	Q71BR3	Q71br3 blackburnia
117	8	1.6	237	2	Q03761	Q03761 nucella lam	190	8	1.6	327	2	Q71BR5	Q71br5 blackburnia
118	8	1.6	238	2	Q03745	Q03745 nucella can	191	8	1.6	327	2	Q71BR6	Q71br6 blackburnia
119	8	1.6	238	2	Q03750	Q03750 nucella fire	192	8	1.6	327	2	Q71BR8	Q71br8 blackburnia
120	8	1.6	238	2	Q03760	Q03760 nucella lam	193	8	1.6	327	2	Q71BU3	Q71bu3 blackburnia
121	8	1.6	238	2	Q9GCH1	Q9gch1 ceratinosto	194	8	1.6	328	2	Q71BT2	Q71bt2 blackburnia
122	8	1.6	238	2	Q9GCH2	Q9gch2 scathophaga	195	8	1.6	329	2	Q71BS1	Q71bs1 blackburnia
123	8	1.6	238	2	Q9GCH3	Q9gch3 scathophaga	196	8	1.6	330	2	Q71BR8	Q71br8 blackburnia
124	8	1.6	238	2	Q9GCH4	Q9gch4 scathophaga	197	8	1.6	332	2	Q71BS0	Q71bs0 blackburnia
125	8	1.6	238	2	Q9GCH5	Q9gch5 scathophaga	198	8	1.6	332	2	Q9B706	Q9b706 eurycea wat
126	8	1.6	238	2	Q9GCH6	Q9gch6 scathophaga	199	8	1.6	333	2	Q71BT1	Q71bt1 blackburnia
127	8	1.6	238	2	Q9GCH7	Q9gch7 scathophaga	200	8	1.6	338	2	Q71BR0	Q71br0 blackburnia
128	8	1.6	238	2	Q9GCH8	Q9gch8 scathophaga	201	8	1.6	338	2	Q71BR2	Q71br2 blackburnia
129	8	1.6	238	2	Q9GCH9	Q9gch9 scathophaga	202	8	1.6	338	2	Q71BR4	Q71br4 blackburnia
130	8	1.6	238	2	Q9GCI0	Q9gci0 scathophaga	203	8	1.6	338	2	Q71BS6	Q71bs6 blackburnia
131	8	1.6	238	2	Q9GCI1	Q9gci1 scathophaga	204	8	1.6	338	2	Q7XWF4	Q7xwf4 oryza sativ
132	8	1.6	238	2	Q9GCI2	Q9gci2 scathophaga	205	8	1.6	339	2	Q7XUH8	Q7xuh8 oryza sativ
133	8	1.6	238	2	Q9GCI3	Q9gci3 scathophaga	206	8	1.6	341	2	Q9B710	Q9b710 eurycea tro
134	8	1.6	238	2	Q9GCI4	Q9gci4 scathophaga	207	8	1.6	342	2	Q21438	Q21438 caenorhabdi
135	8	1.6	238	2	Q9GCI5	Q9gci5 scathophaga	208	8	1.6	358	2	Q71BU7	Q71bu7 blackburnia
136	8	1.6	238	2	Q9GCI6	Q9gci6 scathophaga	209	8	1.6	359	2	Q71BU0	Q71bu0 blackburnia
137	8	1.6	239	2	Q03746	Q03746 nucella can	210	8	1.6	364	2	Q71BT9	Q71bt9 blackburnia
138	8	1.6	239	2	Q03748	Q03748 nucella ema	211	8	1.6	364	2	Q71BU0	Q71bu0 blackburnia
139	8	1.6	239	2	Q03749	Q03749 nucella ema	212	8	1.6	364	2	Q71BU4	Q71bu4 blackburnia
140	8	1.6	239	2	Q03752	Q03752 nucella fire	213	8	1.6	364	2	Q71BU9	Q71bu9 blackburnia
141	8	1.6	239	2	Q03753	Q03753 nucella lim	214	8	1.6	364	2	Q71BV0	Q71bv0 blackburnia
142	8	1.6	239	2	Q03754	Q03754 nucella lim	215	8	1.6	365	1	GLE2_YEAST	P40066 saccharomyc
143	8	1.6	239	2	Q03757	Q03757 nucella lap	216	8	1.6	369	2	Q72KC7	Q72kc7 thermus the
144	8	1.6	239	2	Q03758	Q03758 nucella lam	217	8	1.6	371	2	Q71BU1	Q71bu1 blackburnia
145	8	1.6	239	2	Q03759	Q03759 nucella lim	218	8	1.6	371	2	Q8HQ06	Q8hq06 thrips imag
146	8	1.6	243	2	Q75YF1	Q75ypl nesiohelix	219	8	1.6	372	2	Q6QRA1	Q6qra1 eurycea tyr
147	8	1.6	248	2	Q8M111	Q8m111 harpagifer	220	8	1.6	372	2	Q6QRB9	Q6qrb9 eurycea tyr
148	8	1.6	255	2	Q9B394	Q9b394 blackburnia	221	8	1.6	372	2	Q6QRE2	Q6qre2 eurycea mul
149	8	1.6	257	2	Q8S624	Q8s624 oryza sativ	222	8	1.6	372	2	Q71BU2	Q71bu2 blackburnia
150	8	1.6	258	2	Q7XLL7	Q7xll7 oryza sativ	223	8	1.6	378	1	CYB_ANOQA	P34844 anopheles g
151	8	1.6	260	2	Q9B380	Q9b380 blackburnia	224	8	1.6	378	1	CYB_ANOQU	P33501 anopheles q
152	8	1.6	260	2	Q9B381	Q9b381 blackburnia	225	8	1.6	378	2	Q8MGE0	Q8mge0 barbus trim
153	8	1.6	260	2	Q9B389	Q9b389 blackburnia	226	8	1.6	378	2	Q6B3B1	Q6b3b1 pteronarcys
154	8	1.6	260	2	Q9B391	Q9b391 blackburnia	227	8	1.6	380	1	CYB_CEPNE	Q34179 cepaea nemo
155	8	1.6	260	2	Q9B395	Q9b395 blackburnia	228	8	1.6	380	2	Q9B2C3	Q9b2c3 barbus bigo
156	8	1.6	260	2	Q9B398	Q9b398 blackburnia	229	8	1.6	380	2	Q9G0M6	Q9g0m6 osteoglossu
157	8	1.6	260	2	Q9B3A4	Q9b3a4 blackburnia	230	8	1.6	380	2	Q9G0M7	Q9g0m7 osteoglossu
158	8	1.6	260	2	Q9B3B0	Q9b3b0 blackburnia	231	8	1.6	380	2	Q644A1	Q644a1 bolitoglossu
159	8	1.6	260	2	Q9B3B7	Q9b3b7 blackburnia	232	8	1.6	380	2	Q644K5	Q644k5 desmognathu
160	8	1.6	260	2	Q9B3C2	Q9b3c2 blackburnia	233	8	1.6	380	2	Q645C5	Q645c5 aneides fla
161	8	1.6	260	2	Q9B3C7	Q9b3c7 blackburnia	234	8	1.6	381	2	Q35424	Q35424 protopterus
162	8	1.6	260	2	Q9B3D0	Q9b3d0 blackburnia	235	8	1.6	402	2	Q7TOH3	Q7tdh3 mus musculu
163	8	1.6	260	2	Q9B3D3	Q9b3d3 blackburnia	236	8	1.6	454	2	Q8Y0F1	Q8y0f1 ralstonia s
164	8	1.6	260	2	Q9B3D6	Q9b3d6 blackburnia	237	8	1.6	465	1	NPT1_RABIT	Q28722 o renal sod
165	8	1.6	260	2	Q9B3D9	Q9b3d9 blackburnia	238	8	1.6	465	2	Q8VZY0	Q8vzy0 oryza sativ
166	8	1.6	260	2	Q9B3E2	Q9b3e2 notagonum s	239	8	1.6	476	2	Q8ZZR7	Q8zzr7 pyrobaculum
167	8	1.6	269	2	Q58366	Q58366 pyrococcus	240	8	1.6	479	1	DBPA_BACSU	P42305 bacillus su
168	8	1.6	269	2	Q8U2T4	Q8u2t4 pyrococcus	241	8	1.6	494	2	Q83EH5	Q83eh5 coxiella bu
169	8	1.6	269	2	Q8S691	Q8s691 oryza sativ	242	8	1.6	497	2	Q9Y2C5	Q9y2c5 homo sapien
170	8	1.6	269	2	Q7G785	Q7g785 oryza sativ	243	8	1.6	498	2	Q8VCY5	Q8vcy5 mus musculu
171	8	1.6	269	2	Q7XLO9	Q7xlg9 oryza sativ	244	8	1.6	502	2	Q7XGE6	Q7xge6 oryza sativ
172	8	1.6	269	2	Q851B3	Q851b3 oryza sativ	245	8	1.6	515	2	Q8JFT2	Q8jft2 brachydanio
173	8	1.6	284	2	Q6U0U8	Q6u0u8 oryza sativ	246	8	1.6	535	2	Q7PWK4	Q7pwk4 anopheles g
174	8	1.6	291	2	Q6LHH2	Q6lhh2 oryza sativ	247	8	1.6	560	2	Q6PCD0	Q6pcd0 homo sapien
175	8	1.6	291	2	Q7XKX8	Q7xkx8 oryza sativ	248	8	1.6	560	2	Q9P2U7	Q9p2u7 homo sapien
176	8	1.6	293	2	Q7XK66	Q7xk66 oryza sativ	249	8	1.6	560	2	Q62634	Q62634 rattus norv
177	8	1.6	300	2	Q33966	Q33966 brachylophu	250	8	1.6	576	2	Q6INC8	Q6inc8 xenopus lae

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:34:43 ; Search time 24.9661 Seconds
(without alignments)
1907.682 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSLAPSGEGSDRT.....LFAKGEVQNWALSHQGHNR 495

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR 79:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	2.0	465	2 S69915	sodium-phosphate t
2	10	2.0	544	2 T24633	hypothetical prote
3	10	2.0	573	2 T23589	hypothetical prote
4	9	1.8	380	2 T29248	hypothetical prote
5	9	1.8	395	2 T06132	hypothetical prote
6	8	1.6	138	2 E37587	diacylglycerol kin
7	8	1.6	138	2 AG2808	guaf protein homol
8	8	1.6	269	1 H71107	high-affinity bran
9	8	1.6	308	2 AG0992	high-affinity bran
10	8	1.6	308	2 JH0668	hypothetical prote
11	8	1.6	359	2 T32287	hypothetical prote
12	8	1.6	365	2 S06010	hypothetical prote
13	8	1.6	378	2 T12009	ubiquinol-cytochro
14	8	1.6	378	2 T09812	ubiquinol-cytochro
15	8	1.6	380	2 T11381	ubiquinol-cytochro
16	8	1.6	381	2 S68140	hypothetical prote
17	8	1.6	396	2 T23619	sodium/phosphate t
18	8	1.6	465	2 A56410	ATP-dependent RNA
19	8	1.6	479	2 E69613	brain specific Na+
20	8	1.6	560	2 I59302	hypothetical prote
21	8	1.6	837	2 T12514	two-component hybr
22	8	1.6	1287	2 AF2031	protein kinase (EC
23	8	1.6	4128	2 JG6306	serine proteinase
24	7	1.4	25	2 A60704	dihydroliopamide d
25	7	1.4	33	2 S13863	hypothetical prote
26	7	1.4	44	2 F95124	Sxr (Bkm-homolog)
27	7	1.4	55	2 A21124	vacG protein homol
28	7	1.4	68	2 B64161	holo-(acyl-carrier
29	7	1.4	126	2 F82072	

30	7	1.4	136	2	G97824	50S ribosomal prot
31	7	1.4	140	2	S09525	mercury transport
32	7	1.4	152	2	PT0433	progesterone 11alp
33	7	1.4	153	2	B82330	conserved hypothet
34	7	1.4	165	2	C97624	petP protein limpo
35	7	1.4	165	2	AD2847	transcription regu
36	7	1.4	169	1	OLB04	cytochrome-c oxida
37	7	1.4	172	2	AH2313	phosphatidylglycer
38	7	1.4	182	2	TH7625	hypothetical prote
39	7	1.4	185	2	JK0021	somatotropin - ski
40	7	1.4	187	2	A61123	somatotropin - Moz
41	7	1.4	187	2	PC1082	somatotropin - Jap
42	7	1.4	187	2	JU0030	somatotropin - yel
43	7	1.4	187	2	PC1087	somatotropin - dus
44	7	1.4	187	2	PC1088	somatotropin - gre
45	7	1.4	191	2	S74679	hypothetical prote
46	7	1.4	192	2	AI3437	colicin v producti
47	7	1.4	197	2	A70750	hypothetical prote
48	7	1.4	203	2	S00747	somatotropin precu
49	7	1.4	204	1	STFI	somatotropin precu
50	7	1.4	204	2	A56642	somatotropin precu
51	7	1.4	204	2	I51289	somatotropin - Mor
52	7	1.4	204	2	JN0484	somatotropin precu
53	7	1.4	204	2	JH0577	somatotropin precu
54	7	1.4	204	2	A56904	somatotropin precu
55	7	1.4	204	2	S30431	somatotropin - Aca
56	7	1.4	204	2	JC4261	somatotropin precu
57	7	1.4	212	2	S01746	somatotropin precu
58	7	1.4	212	2	C70898	hypothetical prote
59	7	1.4	225	2	B83083	conserved hypothet
60	7	1.4	231	2	JC6201	GSI protein homolo
61	7	1.4	235	2	S42069	TEGT protein - rat
62	7	1.4	242	2	AE2314	ATP-binding protei
63	7	1.4	247	2	S72859	hypothetical prote
64	7	1.4	252	2	E90184	conserved hypothet
65	7	1.4	252	2	E82040	general secretion
66	7	1.4	279	2	E64109	dimethylsulfoxide
67	7	1.4	279	2	H70855	hypothetical prote
68	7	1.4	282	2	E95128	conserved hypothet
69	7	1.4	282	2	E97999	hypothetical prote
70	7	1.4	284	1	I76721	probable ATP-bindi
71	7	1.4	284	1	S60666	conserved hypothet
72	7	1.4	284	2	AB0906	hypothetical prote
73	7	1.4	284	2	G85984	hypothetical prote
74	7	1.4	284	2	D91139	conserved hypothet
75	7	1.4	284	2	AB0436	conserved hypothet
76	7	1.4	285	2	S74771	hypothetical prote
77	7	1.4	289	1	G64167	hypothetical prote
78	7	1.4	300	2	AE0762	conserved hypothet
79	7	1.4	301	1	H64438	UDP-N-acetylglucos
80	7	1.4	304	2	H75081	phosphate abc tran
81	7	1.4	305	1	H75285	probable ARAC-type
82	7	1.4	307	2	E91206	probable ARAC-type
83	7	1.4	307	2	G86052	hypothetical prote
84	7	1.4	307	2	A65170	hypothetical prote
85	7	1.4	308	2	G98084	hypothetical prote
86	7	1.4	308	2	G95220	hypothetical prote
87	7	1.4	313	2	S11151	amID protein - Str
88	7	1.4	315	2	B71390	NADH2 dehydrogenas
89	7	1.4	315	2	E64426	phosphate transpor
90	7	1.4	316	2	B70768	hypothetical prote
91	7	1.4	317	2	T11337	NADH2 dehydrogenas
92	7	1.4	318	1	QXBO1M	NADH2 dehydrogenas
93	7	1.4	318	2	A58888	NADH2 dehydrogenas
94	7	1.4	318	2	S47870	NADH2 dehydrogenas
95	7	1.4	318	2	T11428	NADH2 dehydrogenas
96	7	1.4	318	2	T11441	NADH2 dehydrogenas
97	7	1.4	318	2	T11140	NADH2 dehydrogenas
98	7	1.4	318	2	T11493	NADH2 dehydrogenas
99	7	1.4	318	2	T11402	NADH2 dehydrogenas
100	7	1.4	318	2	S41835	NADH2 dehydrogenas
101	7	1.4	318	2	S26151	NADH2 dehydrogenas
102	7	1.4	318	2	A58850	NADH2 dehydrogenas

103	7	1.4	318	2	S41820	NADH2 dehydrogenas	176	7	1.4	559	2	S62503	inorganic phosphat
104	7	1.4	318	2	T45550	NADH2 dehydrogenas	177	7	1.4	563	2	T43650	protein sodium-de
105	7	1.4	318	2	T11363	NADH2 dehydrogenas	178	7	1.4	576	2	H88548	protein ZK512.6 [i
106	7	1.4	318	2	T11857	NADH2 dehydrogenas	179	7	1.4	600	2	E48951	nisin transport pr
107	7	1.4	318	2	T11247	NADH2 dehydrogenas	180	7	1.4	635	2	F70874	probable membrane
108	7	1.4	318	2	T10972	NADH2 dehydrogenas	181	7	1.4	640	2	D83571	conserved hypotnet
109	7	1.4	318	2	T11050	NADH2 dehydrogenas	182	7	1.4	644	2	D90940	hypothetical prote
110	7	1.4	321	2	T13811	NADH2 dehydrogenas	183	7	1.4	644	2	G64938	hypothetical prote
111	7	1.4	321	2	S55004	NADH2 dehydrogenas	184	7	1.4	644	2	H85788	hypothetical prote
112	7	1.4	321	2	A50775	probable sugar kin	185	7	1.4	644	2	F82145	conserved hypotnet
113	7	1.4	322	2	S68128	NADH2 dehydrogenas	186	7	1.4	644	2	AF0362	conserved hypotnet
114	7	1.4	323	1	QXLLM	NADH2 dehydrogenas	187	7	1.4	663	2	T47988	serine/threonine-p
115	7	1.4	323	2	T11793	NADH2 dehydrogenas	188	7	1.4	663	2	T38155	78 kd glucose regu
116	7	1.4	323	2	A34284	NADH2 dehydrogenas	189	7	1.4	663	2	S20877	dnak-type molecula
117	7	1.4	323	2	A58892	NADH2 dehydrogenas	190	7	1.4	674	2	I55476	growth potentiati
118	7	1.4	323	2	T09857	NADH2 dehydrogenas	191	7	1.4	678	2	B48089	growth arrest-spec
119	7	1.4	323	2	T11820	NADH2 dehydrogenas	192	7	1.4	682	2	T15092	hypothetical prote
120	7	1.4	324	2	S36002	NADH2 dehydrogenas	193	7	1.4	752	2	G02273	Liv-1 protein - hu
121	7	1.4	324	2	S35462	NADH2 dehydrogenas	194	7	1.4	768	2	T27855	hypothetical prote
122	7	1.4	324	2	T09947	NADH2 dehydrogenas	195	7	1.4	778	2	T17679	proline-rich prote
123	7	1.4	324	2	C41608	NADH2 dehydrogenas	196	7	1.4	781	2	T02272	hypothetical prote
124	7	1.4	324	2	D87075	hypothetical prote	197	7	1.4	792	2	S32244	X-Pro dipeptidyl-p
125	7	1.4	326	1	S41120	cholestenone 5beta	198	7	1.4	847	2	G75270	cation-transportin
126	7	1.4	328	2	T36494	probable membrane	199	7	1.4	860	2	G82310	alanil-tRNA synth
127	7	1.4	330	2	A40602	3',5'-cyclic-nucle	200	7	1.4	877	2	S65057	alpha-glucosidase
128	7	1.4	333	2	E97368	probable enzyme (A	201	7	1.4	909	2	D87434	phosphoenolpyruvat
129	7	1.4	338	2	AD2586	ribosomal RNA smal	202	7	1.4	924	2	S75284	chemotaxis protein
130	7	1.4	343	2	T14245	NADH2 dehydrogenas	203	7	1.4	925	2	E83529	sensor/response re
131	7	1.4	351	2	T19623	hypothetical prote	204	7	1.4	928	2	D72077	polymorphic outer
132	7	1.4	370	2	A80602	probable membrane	205	7	1.4	928	2	H86546	polymorphic outer
133	7	1.4	372	2	S52054	ubiquinol-cytochro	206	7	1.4	949	2	F81591	polymorphic membra
134	7	1.4	372	2	S20056	para-hydroxybenzoa	207	7	1.4	1005	1	P1VXPJ	RNA 1 protein - pe
135	7	1.4	373	2	I37463	acetylserotonin O-	208	7	1.4	1018	2	T15297	hypothetical prote
136	7	1.4	377	2	F95982	probable transport	209	7	1.4	1082	2	T44177	hypothetical prote
137	7	1.4	381	2	T29300	hypothetical prote	210	7	1.4	1082	2	T43990	hypothetical prote
138	7	1.4	384	2	A70805	probable lprn prot	211	7	1.4	1083	2	H86921	probable arabinosy
139	7	1.4	389	2	T10194	hypothetical prote	212	7	1.4	1085	2	F96712	hypothetical prote
140	7	1.4	390	2	T50037	capsular polysacch	213	7	1.4	1086	2	T09325	probable capsid as
141	7	1.4	397	2	S23909	translation elonga	214	7	1.4	1208	2	T05077	hypothetical prote
142	7	1.4	407	2	F70696	hypothetical prote	215	7	1.4	1225	1	B64234	hypothetical prote
143	7	1.4	410	2	S74951	Na+/H+-exchanging	216	7	1.4	1325	1	S73723	probable lipoprote
144	7	1.4	422	2	C82912	phosphoglycerate k	217	7	1.4	1436	2	B81704	conserved hypotnet
145	7	1.4	422	2	A83635	probable O-antigen	218	7	1.4	1516	2	F83085	conserved hypotnet
146	7	1.4	434	2	G83129	probable MFS trans	219	7	1.4	1538	2	B90924	probable ATP-depen
147	7	1.4	436	2	C69764	4-aminobutyrate am	220	7	1.4	1538	2	F85772	ATP-dependent heli
148	7	1.4	443	2	S77166	hypothetical prote	221	7	1.4	1538	2	G64922	probable ATP-depen
149	7	1.4	448	2	T12006	NADH2 dehydrogenas	222	7	1.4	1943	2	B64596	toxin-like outer m
150	7	1.4	452	2	T35729	hypothetical prote	223	7	1.4	1969	2	T08875	histidine kinase h
151	7	1.4	454	2	G70797	hypothetical prote	224	7	1.4	2145	2	S61041	glutamate synthase
152	7	1.4	454	2	T26654	hypothetical prote	225	7	1.4	3194	2	D71917	toxin-like outer m
153	7	1.4	455	2	A82957	probable glutamine	226	7	1.4	15281	2	S41309	cyclosporin synthe
154	7	1.4	460	2	AH0968	sodium,galactoside	227	6	1.2	13	2	D61491	seed protein ws-4
155	7	1.4	461	2	D84971	phosphotransferase	228	6	1.2	17	2	A41053	glutamate receptor
156	7	1.4	462	2	B32840	anthranilate synth	229	6	1.2	18	2	A41877	Lcrkc - yersinia p
157	7	1.4	463	2	B64476	NADP-dependent gly	230	6	1.2	19	2	S69166	ferredoxin b - Jap
158	7	1.4	465	2	I39473	Na+-dependent phos	231	6	1.2	32	2	C61491	seed protein ws-3
159	7	1.4	467	2	A48916	sodium phosphate t	232	6	1.2	35	2	I54460	Qa2 protein - mous
160	7	1.4	472	2	S28286	hypothetical prote	233	6	1.2	39	2	I64027	hypothetical prote
161	7	1.4	473	2	S20612	triacylglycerol li	234	6	1.2	44	2	C35156	dihydrolipoamide d
162	7	1.4	473	2	A38627	gamma-aminobutyric	235	6	1.2	45	2	B35156	dihydrolipoamide d
163	7	1.4	477	2	H83598	probable MFS trans	236	6	1.2	50	2	AE2781	conserved hypotnet
164	7	1.4	479	2	E91195	probable permealase	237	6	1.2	50	2	C97409	hypothetical prote
165	7	1.4	479	2	F86042	probable permealase	238	6	1.2	52	1	S07502	gene 5.9 protein -
166	7	1.4	479	2	C65167	hypothetical 5l.0	239	6	1.2	52	1	S42315	gene 5.9 protein -
167	7	1.4	487	2	F72200	glutamate-tRNA lig	240	6	1.2	55	2	A83500	periplasmic nitrat
168	7	1.4	493	2	G88553	protein C38C10.2 [241	6	1.2	56	2	G72355	hypothetical prote
169	7	1.4	508	2	T05156	probable glucose t	242	6	1.2	57	2	S19088	dihydrolipoamide d
170	7	1.4	515	2	E71447	probable PSII Di p	243	6	1.2	59	2	C81995	hypothetical prote
171	7	1.4	521	2	A53153	glucose transport	244	6	1.2	59	2	F84111	hypothetical prote
172	7	1.4	528	2	AG1937	glucose-6-phosphat	245	6	1.2	60	2	B84811	hypothetical prote
173	7	1.4	531	2	T12406	cytochrome-c oxida	246	6	1.2	61	2	E86084	hypothetical prote
174	7	1.4	539	2	F72288	methyl-accepting c	247	6	1.2	61	2	F96021	hypothetical prote
175	7	1.4	542	1	A70220	phosphotransferase	248	6	1.2	62	2	E89853	hypothetical prote

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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:55:49 ; Search time 106.586 Seconds
(without alignments)
1794.174 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSLAPSGEGSDRT.....LFAKGEVQNAISDHQGRN 495

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1726216 seqs, 386330316 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	495	100.0	495	9	US-09-776-865-4
2	495	100.0	495	17	US-10-823-506-4
3	61	12.3	194	15	US-10-296-115-1200
4	61	12.3	272	15	US-10-264-237-2351
5	61	12.3	284	15	US-10-264-049-2477
6	61	12.3	495	9	US-09-915-181A-7
7	61	12.3	495	16	US-10-755-889-588
8	61	12.3	495	17	US-10-823-506-2
9	61	12.3	536	9	US-09-776-865-2
10	61	12.3	536	17	US-10-823-506-8
11	14	2.8	495	17	US-10-823-506-10

12	14	2.8	495	17	US-10-823-506-12	Sequence 12, Appl
13	12	2.4	78	14	US-10-029-386-27708	Sequence 27708, A
14	11	2.2	578	9	US-09-740-041-4	Sequence 4, Appli
15	11	2.2	578	14	US-10-389-967-4	Sequence 4, Appli
16	11	2.2	582	9	US-09-915-181A-4	Sequence 4, Appli
17	11	2.2	582	15	US-10-205-331-7	Sequence 7, Appl
18	11	2.2	582	16	US-10-734-731-10	Sequence 10, Appl
19	11	2.2	582	16	US-10-734-731-12	Sequence 12, Appl
20	11	2.2	582	16	US-10-734-731-14	Sequence 14, Appl
21	11	2.2	582	16	US-10-807-500-10	Sequence 10, Appl
22	11	2.2	582	16	US-10-807-500-12	Sequence 12, Appl
23	11	2.2	582	16	US-10-807-500-14	Sequence 14, Appl
24	10	2.0	465	9	US-09-915-181A-8	Sequence 8, Appli
25	10	2.0	544	15	US-10-369-493-5873	Sequence 5873, Ap
26	10	2.0	573	15	US-10-369-493-5871	Sequence 5871, Ap
27	10	2.0	573	15	US-10-369-493-5872	Sequence 5872, Ap
28	9	1.8	1803	16	US-10-437-963-188751	Sequence 188751,
29	8	1.6	71	16	US-10-425-115-288336	Sequence 288336,
30	8	1.6	78	16	US-10-437-963-154917	Sequence 154917,
31	8	1.6	93	16	US-10-425-115-366597	Sequence 366597,
32	8	1.6	122	14	US-10-312-187-12	Sequence 12, Appl
33	8	1.6	124	16	US-10-425-115-317259	Sequence 317259,
34	8	1.6	143	16	US-10-425-115-335986	Sequence 335986,
35	8	1.6	232	15	US-10-425-114-43907	Sequence 43907, A
36	8	1.6	235	15	US-10-282-122A-56379	Sequence 56379, A
37	8	1.6	264	15	US-10-108-260A-3281	Sequence 3281, Ap
38	8	1.6	269	16	US-10-437-963-130004	Sequence 130004,
39	8	1.6	276	16	US-10-437-963-138193	Sequence 138193,
40	8	1.6	283	16	US-10-437-963-154806	Sequence 154806,
41	8	1.6	291	16	US-10-437-963-156500	Sequence 156500,
42	8	1.6	337	16	US-10-437-963-195084	Sequence 195084,
43	8	1.6	360	15	US-10-282-122A-45021	Sequence 45021, A
44	8	1.6	365	13	US-10-084-700-32	Sequence 32, Appl
45	8	1.6	365	15	US-10-369-493-1761	Sequence 1761, Ap
46	8	1.6	384	15	US-10-424-599-183068	Sequence 183068,
47	8	1.6	391	16	US-10-437-963-141744	Sequence 141744,
48	8	1.6	448	16	US-10-437-963-125768	Sequence 125768,
49	8	1.6	455	16	US-10-437-963-138196	Sequence 138196,
50	8	1.6	478	16	US-10-437-963-180400	Sequence 180400,
51	8	1.6	479	15	US-10-369-493-23364	Sequence 23364, A
52	8	1.6	484	16	US-10-437-963-138203	Sequence 138203,
53	8	1.6	488	16	US-10-437-963-130220	Sequence 130220,
54	8	1.6	493	16	US-10-437-963-124551	Sequence 124551,
55	8	1.6	495	16	US-10-437-963-141738	Sequence 141738,
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57	8	1.6	556	16	US-10-437-963-113498	Sequence 113498,
58	8	1.6	560	9	US-09-991-212A-4	Sequence 4, Appli
59	8	1.6	560	9	US-09-915-181A-5	Sequence 5, Appli
60	8	1.6	560	10	US-09-965-522-4	Sequence 4, Appli
61	8	1.6	560	15	US-10-314-790-5	Sequence 4, Appli
62	8	1.6	560	16	US-10-734-731-2	Sequence 2, Appli
63	8	1.6	560	16	US-10-734-731-4	Sequence 4, Appli
64	8	1.6	560	16	US-10-734-731-6	Sequence 6, Appli
65	8	1.6	560	16	US-10-734-731-8	Sequence 8, Appli
66	8	1.6	560	16	US-10-807-500-2	Sequence 2, Appli
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69	8	1.6	560	16	US-10-807-500-8	Sequence 8, Appli
70	8	1.6	560	17	US-10-877-818-4	Sequence 8, Appli
71	8	1.6	561	16	US-10-437-963-188694	Sequence 188694,
72	8	1.6	566	15	US-10-287-226-300	Sequence 300, App
73	8	1.6	580	16	US-10-437-963-146162	Sequence 146162,
74	8	1.6	589	9	US-09-740-041-2	Sequence 2, Appli
75	8	1.6	589	14	US-10-389-967-2	Sequence 2, Appli
76	8	1.6	589	18	US-10-499-731-28	Sequence 28, Appl
77	8	1.6	594	16	US-10-437-963-138200	Sequence 138200,
78	8	1.6	601	16	US-10-499-731-46	Sequence 46, Appl
79	8	1.6	618	16	US-10-437-963-195088	Sequence 195088,
80	8	1.6	642	16	US-10-437-963-164012	Sequence 164012,
81	8	1.6	643	16	US-10-437-963-124148	Sequence 124148,
82	8	1.6	652	16	US-10-437-963-124155	Sequence 124155,
83	8	1.6	656	16	US-10-437-963-141761	Sequence 141761,
84	8	1.6	656	16	US-10-437-963-141769	Sequence 141769,

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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:46:03 ; Search time 28.807 Seconds
(without alignments)
1282.720 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSLAPSDGEGSDRT.....LFAKGEVQNWAISDQGRN 495

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	61	12.3	495	US-09-359-167-2	Sequence 2, Appli
3	61	12.3	495	US-09-915-181A-7	Sequence 7, Appli
4	61	12.3	495	US-09-359-167-8	Sequence 8, Appli
5	61	12.3	585	US-09-949-016-7705	Sequence 7705, Ap
6	14	2.8	495	US-09-359-167-10	Sequence 10, Appl
7	14	2.8	495	US-09-359-167-12	Sequence 12, Appl
8	12	2.4	436	US-09-949-016-11448	Sequence 11448, A
9	12	2.4	470	US-08-724-394A-10	Sequence 10, Appl
10	11	2.2	578	US-09-740-041-4	Sequence 4, Appli
11	11	2.2	582	US-09-915-181A-8	Sequence 4, Appli
12	10	2.0	465	US-09-915-181A-4	Sequence 8, Appli
13	8	1.6	140	US-09-270-767-33069	Sequence 33069, A
14	8	1.6	140	US-09-270-767-48286	Sequence 48286, A
15	8	1.6	171	US-09-902-540-15679	Sequence 15679, A
16	8	1.6	234	US-09-252-991A-28420	Sequence 28420, A
17	8	1.6	367	US-09-328-352-6126	Sequence 6126, Ap
18	8	1.6	380	US-09-949-016-7053	Sequence 7053, Ap
19	8	1.6	401	US-09-328-352-6962	Sequence 6962, Ap
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22	8	1.6	560	US-08-647-481-2	Sequence 2, Appli
23	8	1.6	560	US-08-430-033A-2	Sequence 2, Appli
24	8	1.6	560	US-08-805-118-4	Sequence 4, Appli
25	8	1.6	560	US-09-391-958-4	Sequence 4, Appli
26	8	1.6	560	US-09-915-181A-5	Sequence 5, Appli
27	8	1.6	560	PCT-US96-05792-2	Sequence 2, Appli

28	8	1.6	567	4	US-09-949-016-11354	Sequence 11354, A
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32	7	1.4	91	4	US-09-543-681A-8118	Sequence 8118, Ap
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34	7	1.4	96	4	US-09-252-991A-16613	Sequence 16613, A
35	7	1.4	102	4	US-09-710-279-2592	Sequence 2592, Ap
36	7	1.4	110	4	US-09-248-796A-14320	Sequence 14320, A
37	7	1.4	122	3	US-09-134-001C-4987	Sequence 4987, Ap
38	7	1.4	135	4	US-09-252-991A-25112	Sequence 25112, A
39	7	1.4	140	1	US-08-133-347-5	Sequence 5, Appli
40	7	1.4	142	4	US-09-949-016-7180	Sequence 7180, Ap
41	7	1.4	157	4	US-09-673-395A-267	Sequence 267, App
42	7	1.4	157	4	US-09-270-767-44201	Sequence 44201, A
43	7	1.4	163	4	US-09-270-767-32926	Sequence 32926, A
44	7	1.4	163	4	US-09-270-767-48143	Sequence 48143, A
45	7	1.4	177	4	US-09-489-039A-11522	Sequence 11522, A
46	7	1.4	187	3	US-09-194-185-1	Sequence 1, Appli
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48	7	1.4	204	4	US-09-549-831-6	Sequence 6, Appli
49	7	1.4	212	4	US-09-934-901-10	Sequence 10, Appl
50	7	1.4	212	4	US-09-934-868-20	Sequence 20, Appl
51	7	1.4	212	4	US-09-248-796A-20354	Sequence 20354, A
52	7	1.4	212	4	US-10-321-210-10	Sequence 10, Appl
53	7	1.4	212	4	US-10-320-874-10	Sequence 10, Appl
54	7	1.4	225	4	US-09-252-991A-29348	Sequence 29348, A
55	7	1.4	225	4	US-09-270-767-45231	Sequence 45231, A
56	7	1.4	228	4	US-09-540-236-2798	Sequence 2798, Ap
57	7	1.4	279	3	US-08-549-515-7	Sequence 7, Appli
58	7	1.4	282	4	US-09-583-110-3800	Sequence 3800, Ap
59	7	1.4	287	4	US-09-107-433-4120	Sequence 4120, Ap
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61	7	1.4	297	4	US-09-252-991A-24412	Sequence 24412, A
62	7	1.4	301	4	US-09-902-540-15018	Sequence 15018, A
63	7	1.4	306	4	US-09-134-000C-4155	Sequence 4155, Ap
64	7	1.4	307	4	US-09-522-714-16	Sequence 16, Appl
65	7	1.4	307	4	US-09-489-039A-10116	Sequence 10116, A
66	7	1.4	308	4	US-09-583-110-2950	Sequence 2950, Ap
67	7	1.4	310	4	US-09-543-681A-6311	Sequence 6311, Ap
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69	7	1.4	311	4	US-09-489-039A-9786	Sequence 9786, Ap
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75	7	1.4	351	4	US-09-636-728-28	Sequence 28, Appl
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104	7	1.4	678	1	US-08-435-436-2	Sequence 2, Appli	177	6	1.2	68	4	US-09-513-999C-4902	Sequence 4902, Ap
105	7	1.4	678	2	US-08-438-863-2	Sequence 2, Appli	178	6	1.2	69	4	US-09-248-796A-14723	Sequence 14723, A
106	7	1.4	678	2	US-08-438-864-2	Sequence 2, Appli	179	6	1.2	70	4	US-09-489-039A-10796	Sequence 10796, A
107	7	1.4	678	3	US-08-438-862-2	Sequence 2, Appli	180	6	1.2	70	4	US-09-621-976-6964	Sequence 6964, Ap
108	7	1.4	678	3	US-08-628-747-2	Sequence 2, Appli	181	6	1.2	72	4	US-09-248-796A-21901	Sequence 21901, A
109	7	1.4	678	3	US-08-402-253-2	Sequence 2, Appli	182	6	1.2	72	4	US-09-248-796A-27413	Sequence 27413, A
110	7	1.4	678	3	US-08-443-866B-2	Sequence 2, Appli	183	6	1.2	73	4	US-09-107-532A-4574	Sequence 4574, Ap
111	7	1.4	722	4	US-09-252-991A-17407	Sequence 17407, A	184	6	1.2	74	4	US-09-621-976-7165	Sequence 7165, AP
112	7	1.4	755	4	US-09-642-034-5	Sequence 5, Appli	185	6	1.2	74	4	US-09-270-767-40827	Sequence 40827, A
113	7	1.4	832	4	US-09-252-991A-17267	Sequence 17267, A	186	6	1.2	74	4	US-09-270-767-56043	Sequence 56043, A
114	7	1.4	834	4	US-09-404-967C-5	Sequence 5, Appli	187	6	1.2	75	3	US-08-817-811-97	Sequence 97, Appli
115	7	1.4	850	4	US-09-328-352-7660	Sequence 7660, Ap	188	6	1.2	75	4	US-09-788-006-169	Sequence 169, App
116	7	1.4	859	5	PCT-US95-580-2	Sequence 2, Appli	189	6	1.2	75	4	US-09-902-540-12774	Sequence 12774, A
117	7	1.4	859	5	PCT-US95-02792-2	Sequence 2, Appli	190	6	1.2	75	4	US-09-902-540-13864	Sequence 13864, A
118	7	1.4	877	1	US-08-430-925A-4	Sequence 4, Appli	191	6	1.2	76	3	US-08-817-811-21	Sequence 21, Appli
119	7	1.4	891	4	US-09-949-016-7798	Sequence 7798, Ap	192	6	1.2	77	4	US-09-489-039A-9235	Sequence 9235, Ap
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121	7	1.4	947	4	US-09-252-991A-29359	Sequence 29359, A	194	6	1.2	77	4	US-09-489-039A-11231	Sequence 11231, A
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134	7	1.4	1374	4	US-08-588-985-2	Sequence 2, Appli	207	6	1.2	81	4	US-09-107-433-2805	Sequence 2805, Ap
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136	7	1.4	1865	4	US-09-949-016-6069	Sequence 6069, Ap	209	6	1.2	83	3	US-09-134-001C-4659	Sequence 4659, Ap
137	7	1.4	3647	4	US-09-949-016-10932	Sequence 10932, A	210	6	1.2	83	4	US-09-489-039A-10406	Sequence 10406, A
138	7	1.4	15281	2	US-08-471-119A-2	Sequence 7, Appli	211	6	1.2	83	4	US-09-248-796A-25200	Sequence 25200, A
139	6	1.2	6	5	PCT-US92-01433A-7	Sequence 7, Appli	212	6	1.2	84	4	US-09-489-039A-9870	Sequence 9870, Ap
140	6	1.2	10	4	US-09-653-465B-11	Sequence 11, Appl	213	6	1.2	85	2	US-08-479-078-12	Sequence 12, Appl
141	6	1.2	10	4	US-09-191-593-41	Sequence 41, Appl	214	6	1.2	85	4	US-09-252-991A-19059	Sequence 19059, A
142	6	1.2	12	4	US-10-118-575A-18	Sequence 18, Appl	215	6	1.2	88	4	US-09-248-796A-15960	Sequence 15960, A
143	6	1.2	13	4	US-09-190-976B-12	Sequence 12, Appl	216	6	1.2	89	4	US-09-107-532A-6179	Sequence 6179, Ap
144	6	1.2	16	2	US-08-642-406A-12	Sequence 12, Appl	217	6	1.2	90	4	US-09-270-767-39428	Sequence 39428, A
145	6	1.2	16	3	US-09-199-534-12	Sequence 12, Appl	218	6	1.2	90	4	US-09-270-767-54645	Sequence 54645, A
146	6	1.2	16	4	US-09-199-534-12	Sequence 12, Appl	219	6	1.2	91	4	US-09-270-767-31960	Sequence 31960, A
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151	6	1.2	34	1	US-07-745-206A-5	Sequence 5, Appli	224	6	1.2	95	4	US-09-489-039A-9597	Sequence 9597, Ap
152	6	1.2	34	1	US-08-455-543A-50	Sequence 50, Appl	225	6	1.2	95	4	US-09-270-767-40845	Sequence 40845, A
153	6	1.2	34	2	US-08-223-305C-50	Sequence 50, Appl	226	6	1.2	95	4	US-09-270-767-56061	Sequence 56061, A
154	6	1.2	34	2	US-08-311-363-5	Sequence 5, Appli	227	6	1.2	96	4	US-09-746-801A-41	Sequence 41, Appl
155	6	1.2	36	2	US-08-846-762-59	Sequence 59, Appl	228	6	1.2	96	4	US-09-270-767-61787	Sequence 61787, A
156	6	1.2	40	4	US-09-602-777A-12	Sequence 12, Appl	229	6	1.2	96	4	US-09-513-999C-6655	Sequence 6655, Ap
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168	6	1.2	59	4	US-09-270-767-41846	Sequence 41846, A	241	6	1.2	104	3	US-08-744-419-2	Sequence 2, Appli
169	6	1.2	59	4	US-09-270-767-57088	Sequence 57088, A	242	6	1.2	104	4	US-09-545-894-4	Sequence 4, Appli
170	6	1.2	61	4	US-09-248-796A-24784	Sequence 24784, A	243	6	1.2	104	4	US-09-270-767-57166	Sequence 57166, A
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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:29:52 ; Search time 108.026 Seconds
(without alignments)
1772.222 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSLAPSGEGSDRT.....LFAKGEVQNWALSDHQGRN 495

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A Genesep16Dec04:*

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	495	100.0	495	3	AAY45088 Sheep GBS
2	495	100.0	495	4	AAB06519 Sheep gro
3	61	12.3	124	4	AG81307 Human AFP
4	61	12.3	194	4	AAM25685 Human pro
5	61	12.3	272	5	ABB89975 Human pro
6	61	12.3	284	5	ABP41345 Human ova
7	61	12.3	314	4	ASG65238 Human sod
8	61	12.3	495	3	AAY45087 Partial h
9	61	12.3	495	4	AAB66967 Human AST
10	61	12.3	495	4	AAM38959 Human pol
11	61	12.3	495	8	ADJ75516 Marker ge
12	61	12.3	495	8	ADR14587 Human NF-
13	61	12.3	495	8	ADP25217 PRO polyp
14	61	12.3	536	3	AAY45089 Human GBS
15	61	12.3	536	4	AAB06518 Human gro
16	32	6.5	277	4	AAM93914 Human pol
17	32	6.5	277	8	ADL32036 Human pro
18	32	6.5	309	4	AAM40745 Human pol
19	29	5.9	256	4	ABG02032 Novel hum
20	29	5.9	343	4	ABG12999 Novel hum
21	29	5.9	343	6	ABO00820 Polypepti
22	15	3.0	15	4	AG65239 Human sod
23	14	2.8	495	3	AAY45090 Human/She
24	12	2.4	78	8	ABO54074 Human gen
25	12	2.4	436	2	AAW78919 Human hae

26	12	2.4	436	7	ADF90914	Human hep
27	12	2.4	559	4	ABB58701	Drosophil
28	11	2.2	578	7	ADG88331	Rat trans
29	11	2.2	582	4	AAW79273	Human pro
30	11	2.2	582	6	ABG74796	Rat DNPI
31	11	2.2	582	6	ABG74795	Human DNP
32	11	2.2	582	6	ABG74797	Murine DN
33	11	2.2	582	6	ABM04787	Rat Na-de
34	11	2.2	582	7	ADC15494	Mouse DNP
35	11	2.2	582	7	ADC15492	Rat DNPI
36	11	2.2	582	7	ADC15490	Human DNP
37	11	2.2	582	7	ADD01475	Human VGL
38	10	2.0	387	8	ADP29764	Human sec
39	10	2.0	497	4	ABB70142	Drosophil
40	10	2.0	502	4	ABB65873	Drosophil
41	10	2.0	502	4	ABB60525	Drosophil
42	10	2.0	544	8	ADN23220	Bacterial
43	10	2.0	573	8	ADN23219	Bacterial
44	10	2.0	573	8	ADN23218	Bacterial
45	9	1.8	363	3	AAO83399	Arabidops
46	9	1.8	384	3	AAO83398	Arabidops
47	9	1.8	462	4	ABB70143	Drosophil
48	8	1.6	79	2	RAY59932	Human myo
49	8	1.6	122	5	AAU81759	Partial p
50	8	1.6	234	7	ABO79674	Pseudomon
51	8	1.6	235	6	ABU28455	Protein e
52	8	1.6	264	7	ADM04596	Human pro
53	8	1.6	273	8	ADN46581	Thermococ
54	8	1.6	360	6	ABU17097	Protein e
55	8	1.6	365	6	ABR53883	Protein s
56	8	1.6	365	7	ADK63542	Disease t
57	8	1.6	365	8	ADN13108	Bacterial
58	8	1.6	367	6	ADA34839	Acinetoba
59	8	1.6	401	6	ADA35675	Acinetoba
60	8	1.6	479	8	ADS44934	Bacterial
61	8	1.6	560	2	AAW05148	Human bra
62	8	1.6	560	2	AAW70500	Human sod
63	8	1.6	560	6	ABG74794	Murine BN
64	8	1.6	560	6	ABG74793	Rat BNPI
65	8	1.6	560	6	ABG74792	Human BNP
66	8	1.6	560	6	ABG74791	Human BNP
67	8	1.6	560	7	ADC15488	Mouse BNP
68	8	1.6	560	7	ADC15484	Human BNP
69	8	1.6	560	7	ADC15482	Human BNP
70	8	1.6	560	7	ADC15486	Rat BNPI
71	8	1.6	560	7	ADD01474	Human VGL
72	8	1.6	566	7	ADJ95072	Novel NOV
73	8	1.6	567	4	AAO13870	Human pol
74	8	1.6	589	5	AAU93329	Human tra
75	8	1.6	589	5	AAO30994	Human tra
76	8	1.6	589	7	ADD01392	Human TCH
77	8	1.6	589	7	ADG88329	Human tra
78	8	1.6	589	8	ADR10021	Human pro
79	8	1.6	601	7	ADD01410	Mouse TCH
80	8	1.6	835	5	AAU81754	Human clk
81	8	1.6	837	8	ABM81694	Tumour-as
82	8	1.6	860	5	ABO76889	Rat gluta
83	8	1.6	874	6	ABU65243	Novel hum
84	8	1.6	2015	4	ABG65890	Drosophil
85	8	1.6	4128	7	ADB85120	Mouse DNA
86	7	1.4	14	3	ADC16844	Human sin
87	7	1.4	19	7	ADC39960	Yellow gr
88	7	1.4	22	8	ADJ79763	Subunit I
89	7	1.4	22	8	ADN12017	Subunit I
90	7	1.4	24	7	ADP76655	Novel hum
91	7	1.4	31	4	ABG12078	Novel hum
92	7	1.4	31	4	ABG13776	Novel hum
93	7	1.4	32	2	AAU86113	S. pneumo
94	7	1.4	34	3	AAU89268	Gene 13 h
95	7	1.4	40	5	AAU89268	Insulin/i
96	7	1.4	40	6	ABJ25329	SAC isola
97	7	1.4	44	3	ABJ25329	Human sec
98	7	1.4	44	5	AAU90770	Insulin/i

99	7	1.4	44	6	ABU01493	Abu01493 S. pneumo	172	7	1.4	207	2	AAR05800	Aar05800 Tilapia (
100	7	1.4	76	4	ABU65452	Aau65452 Propionib	173	7	1.4	207	2	AAR08122	Aar08122 Tilapia g
101	7	1.4	76	4	ABM61971	Abm61971 Propionib	174	7	1.4	207	5	ABB89411	Abb89411 Human pol
102	7	1.4	81	5	ABP08020	Abp08020 Human ORF	175	7	1.4	212	5	ABB09165	Abb09165 Methylo
103	7	1.4	91	7	ADP07833	Adp07833 Bacterial	176	7	1.4	212	5	ABE22300	Aae22300 Methylo
104	7	1.4	96	7	ABO67867	AbO67867 Pseudomon	177	7	1.4	212	5	ABG51560	Abg51560 High grow
105	7	1.4	99	4	AAU30972	Aau30972 Novel hum	178	7	1.4	212	5	ABU05797	Abu05797 M. tuberc
106	7	1.4	102	4	AAg82749	Ag82749 S. epider	179	7	1.4	222	2	ABM68944	Abm68944 Photothab
107	7	1.4	103	6	ADA54545	Ada54545 Human tra	180	7	1.4	222	2	AAb56768	Aab56768 Human pro
108	7	1.4	107	5	ADP35197	Adp35197 Human tra	181	7	1.4	223	3	AAO15070	Aao15070 Humicola
109	7	1.4	110	4	AAm91463	Aam91463 Human imm	182	7	1.4	223	5	AAg80602	Aag80602 Humicola
110	7	1.4	111	5	ASP31660	Asp31660 Human ORF	183	7	1.4	225	7	ABO80602	AbO80602 Pseudomon
111	7	1.4	115	8	ADR66927	Adr66927 Human pro	184	7	1.4	227	4	ABG16682	Abg16682 Novel hum
112	7	1.4	115	8	ADR66029	Adr66029 Human pro	185	7	1.4	228	5	AAO15062	Aao15062 Endogluca
113	7	1.4	122	5	ABP40142	Abp40142 Staphyloc	186	7	1.4	228	8	ADL05112	Adl05112 M. catarr
114	7	1.4	122	8	ADSO7186	Adso7186 Staphyloc	187	7	1.4	231	4	ABB70615	Abb70615 Drosophil
115	7	1.4	126	6	ABU49557	Abu49557 Protein e	188	7	1.4	231	8	ADN48262	Adn48262 Thermoco
116	7	1.4	132	4	ABE59519	Ab59519 Human sec	189	7	1.4	264	8	ADI19308	Adi19308 Ag2/PRAL-
117	7	1.4	132	7	ADM25718	Adm25718 Hyperther	190	7	1.4	266	6	ABP75751	Abp75751 Human sec
118	7	1.4	133	4	ABE68834	Ab68834 Drosophil	191	7	1.4	270	4	ADQ90464	Adq90464 T tengcon
119	7	1.4	135	7	ABO76366	AbO76366 Pseudomon	192	7	1.4	270	8	ADH45300	Adh45300 Human enz
120	7	1.4	136	7	ADM04743	Adm04743 Human pro	193	7	1.4	279	3	AAy88627	Aay88627 H. influe
121	7	1.4	136	8	ADQ96242	Adq96242 T cell ac	194	7	1.4	279	5	ABU05927	Abu05927 M. tuberc
122	7	1.4	145	2	AAW94926	Aaw94926 Human phe	195	7	1.4	282	6	ABU01530	Abu01530 S. pneumo
123	7	1.4	146	8	ADS17938	AdS17938 Coccidioi	196	7	1.4	282	6	ABP81392	Abp81392 Streptoco
124	7	1.4	147	4	AAW43546	Aam43546 Human pol	197	7	1.4	282	6	ABU44997	Abu44997 Streptoc
125	7	1.4	147	4	AAU19939	Aau19939 Novel hum	198	7	1.4	282	8	ADK47285	Adk47285 Streptoco
126	7	1.4	147	4	AAU87555	Aau87555 Novel cen	199	7	1.4	282	8	ADM92159	Adm92159 S pneumon
127	7	1.4	147	8	ADI54870	Adi54870 Novel hum	200	7	1.4	284	4	AAU38138	Aau38138 Salmonell
128	7	1.4	147	8	ADM24567	Adm24567 Human PRO	201	7	1.4	284	4	AAU34730	Aau34730 E. coli c
129	7	1.4	155	3	AAE53291	AAE53291 Human col	202	7	1.4	284	6	ABM68248	Abm68248 Photothab
130	7	1.4	155	3	AAE24501	AAE24501 Human col	203	7	1.4	284	6	ABU50326	Abu50326 Protein e
131	7	1.4	155	4	AAAG74756	AAg74756 Human col	204	7	1.4	284	6	ABU28786	Abu28786 Protein e
132	7	1.4	157	2	AAV60067	Aay60067 Human end	205	7	1.4	284	6	ABU40658	Abu40658 Protein e
133	7	1.4	161	6	ABU20231	Abu20231 Protein e	206	7	1.4	284	6	ABU47130	Abu47130 Protein e
134	7	1.4	163	3	AGI13183	Ag13183 Arabidops	207	7	1.4	284	6	ABU28308	Abu28308 Protein e
135	7	1.4	166	8	ADS17940	AdS17940 Coccidioi	208	7	1.4	284	6	ABU31668	Abu31668 Protein e
136	7	1.4	171	3	AAE13182	Ag13182 Arabidops	209	7	1.4	284	6	ABU47728	Abu47728 Protein e
137	7	1.4	172	3	AAE56835	AAE56835 Human pro	210	7	1.4	287	8	ADR95485	Adr95485 Novel S.
138	7	1.4	172	6	ABG99987	Abg99987 Human nov	211	7	1.4	289	4	AAU35600	Aau35600 Haemophil
139	7	1.4	173	7	ADM26716	Adm26716 Hyperther	212	7	1.4	289	6	ABU30505	Abu30505 Protein e
140	7	1.4	175	6	ABP78104	Abp78104 N. gonorr	213	7	1.4	291	7	ABO79826	AbO79826 Pseudomon
141	7	1.4	177	7	ABO65005	ABO65005 Klebsstei	214	7	1.4	294	2	AAW70319	Aaw70319 Secreted
142	7	1.4	185	1	AAAP90694	AAp90694 Sequence	215	7	1.4	294	2	ABO84924	ABO84924 Human can
143	7	1.4	185	7	ADC39950	AdC39950 Yellow gr	216	7	1.4	295	2	AAy25758	Aay25758 Human sec
144	7	1.4	186	1	AAAP90616	AAp90616 Fish grow	217	7	1.4	297	7	ABO75666	AbO75666 Pseudomon
145	7	1.4	187	1	AAE81244	AAE81244 Sequence	218	7	1.4	301	8	ADN47594	Adn47594 Thermoco
146	7	1.4	187	2	AAW71372	Aaw71372 Synthetic	219	7	1.4	302	8	ADL57159	Adl57159 Human NOV
147	7	1.4	187	2	AAW49019	Aam49019 Korean ro	220	7	1.4	303	6	ABU24928	Abu24928 Protein e
148	7	1.4	188	2	AAW07353	Aar07353 Fish grow	221	7	1.4	304	4	AAAB96280	Aab96280 Putative
149	7	1.4	188	2	AAW24137	Aar24137 Fish grow	222	7	1.4	304	5	ABP30465	ABP30465 Streptoco
150	7	1.4	192	4	AAE61301	AAE61301 Human tra	223	7	1.4	304	7	ADM05529	Adm05529 Human pro
151	7	1.4	192	5	ABB09599	Abb09599 Human pal	224	7	1.4	306	5	ABP27232	Abp27232 Streptoco
152	7	1.4	192	8	ADQ96240	Adq96240 T cell ac	225	7	1.4	306	7	ADH86270	Adh86270 Enteroco
153	7	1.4	192	8	ADQ96136	Adq96136 T cell ac	226	7	1.4	307	3	AAH18901	AAH18901 A maize c
154	7	1.4	200	1	AAAP90732	AAp90732 Fish grow	227	7	1.4	307	4	ABG12674	Abg12674 Novel hum
155	7	1.4	200	4	AAE59504	AAE59504 Human sec	228	7	1.4	307	7	ABO63599	ABO63599 Klebsstei
156	7	1.4	200	7	ADC86463	AdC86463 Human GPC	229	7	1.4	308	4	AAm01075	Aam01075 CPE 78 pr
157	7	1.4	201	4	ABG13795	ABg13795 Novel hum	230	7	1.4	308	5	ABP25574	Abp25574 Streptoco
158	7	1.4	202	4	ABE63463	ABe63463 Drosophil	231	7	1.4	308	6	ABU02385	Abu02385 S. pneumo
159	7	1.4	203	1	AAAP90617	AAp90617 Fish grow	232	7	1.4	308	6	ABP81461	ABP81461 Streptoco
160	7	1.4	203	2	AAW07248	Aar07248 Fish grow	233	7	1.4	308	8	ADK46435	Adk46435 Streptoco
161	7	1.4	203	3	AAU77282	Aau77282 Spotted f	234	7	1.4	308	8	ADM92229	Adm92229 S pneumon
162	7	1.4	204	1	AAAP95638	AAp95638 Fish grow	235	7	1.4	308	8	ADR83899	Adr83899 S. pyogen
163	7	1.4	204	2	AAW10912	Aar10912 Fish grow	236	7	1.4	310	7	ADF06026	Adf06026 Bacterial
164	7	1.4	204	2	AAW27340	Aaw27340 Yellow ta	237	7	1.4	311	7	ABO63269	ABO63269 Klebsstei
165	7	1.4	204	2	AAW25120	Aaw25120 Yellowtai	238	7	1.4	311	8	ADR94722	Adr94722 Novel S.
166	7	1.4	204	2	AAW49020	Aam49020 Korean ro	239	7	1.4	315	8	ADR09349	Adr09349 Human pro
167	7	1.4	204	5	ABG31737	ABg31737 Yellow gr	240	7	1.4	323	8	ADS43275	AdS43275 Bacterial
168	7	1.4	204	5	ABG31734	ABg31734 Yellow gr	241	7	1.4	326	4	AAU34980	Aau34980 Enteroco
169	7	1.4	204	7	ADB64099	AdB64099 Human pro	242	7	1.4	326	6	ABO07155	ABO07155 Novel hum
170	7	1.4	204	7	ADC50041	AdC50041 Orange-sp	243	7	1.4	326	6	ABU29293	Abu29293 Protein e
171	7	1.4	204	7	ADC39941	AdC39941 Yellow gr	244	7	1.4	326	7	ADF90912	Adf90912 Human hep

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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:30:47 ; Search time 119.573 Seconds
(without alignments)
2295.451 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 536

Sequence: 1: MAAGANTPPRPVQPARPGGF.....LFAKGEVQNALNDHGHRRH 536

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495	92.4	495	1	S175 HUMAN
2	61	11.4	495	1	S175 SHEEP
3	34	6.3	495	1	S175 MOUSE
4	11	2.1	157	2	Q96KL7
5	11	2.1	465	1	NPT1 HUMAN
6	11	2.1	467	2	Q9H531
7	11	2.1	582	2	Q9P2U8
8	11	2.1	582	2	Q920B7
9	11	2.1	582	2	Q8BLE7
10	11	2.1	582	2	Q9J112
11	10	1.9	172	2	Q7PWK3
12	10	1.9	363	2	Q8BWS1
13	10	1.9	436	1	NPT3 HUMAN
14	10	1.9	447	2	Q8VCX8
15	10	1.9	466	2	Q96LH1
16	10	1.9	535	2	Q7PWK4
17	10	1.9	544	1	YRT3 CAEEL
18	10	1.9	573	2	Q09932
19	9	1.7	69	2	Q91Y99
20	9	1.7	127	2	Q71118
21	9	1.7	286	2	Q7PRG4
22	9	1.7	390	2	Q921B2
23	9	1.7	465	1	NPT1 MOUSE
24	9	1.7	465	1	NPT1 RAT
25	9	1.7	465	2	Q8K3H3
26	9	1.7	465	2	Q91WV5
27	9	1.7	465	2	Q6AZ46
28	9	1.7	469	2	Q8CJH8
29	9	1.7	475	2	Q6AZ69
30	9	1.7	497	2	Q8MRP7
31	9	1.7	498	2	Q8CJH9

32	9	1.7	715	2	O83248	O83248 treponema p
33	8	1.5	10	2	O7S377	O7S377 neurospora
34	8	1.5	126	2	Q9LRG3	Q9LRG3 chlorella v
35	8	1.5	250	1	HXB9_MOUSE	P20615 mus musculus
36	8	1.5	255	2	O99909	O99909 potamogeton
37	8	1.5	296	2	Q97CJ3	Q97CJ3 thermoplasma
38	8	1.5	308	1	LIVH_SALTY	P30295 salmonella
39	8	1.5	342	2	Q21438	Q21438 caenorhabdi
40	8	1.5	369	2	Q72KC7	Q72KC7 thermus the
41	8	1.5	373	2	O53550	O53550 mycobacteri
42	8	1.5	373	2	Q7TWC6	Q7TWC6 mycobacteri
43	8	1.5	376	2	Q674M9	Q674M9 trialeurode
44	8	1.5	398	2	O9ZDV1	O9ZDV1 rickettsia
45	8	1.5	402	2	O7TQH3	O7TQH3 mus musculu
46	8	1.5	465	1	NFT1_RABIT	Q28722 o renal sod
47	8	1.5	470	2	Q7YTZ7	Q7YTZ7 drosophila
48	8	1.5	476	2	Q8ZZR7	Q8ZZR7 pyrobaculum
49	8	1.5	476	2	Q7Q579	Q7Q579 anopheles g
50	8	1.5	479	1	DBPA_BACSU	P42305 bacillus su
51	8	1.5	479	2	Q23514	Q23514 caenorhabdi
52	8	1.5	497	2	Q9Y2C5	Q9Y2C5 homo sapien
53	8	1.5	497	2	Q6NR28	Q6NR28 drosophila
54	8	1.5	497	2	Q7KRJ1	Q7KRJ1 drosophila
55	8	1.5	498	2	Q8VCY5	Q8VCY5 mus musculu
56	8	1.5	502	2	Q9VDM0	Q9VDM0 drosophila
57	8	1.5	515	2	Q8JFT2	Q8JFT2 brachydanio
58	8	1.5	533	2	Q7Q1S5	Q7Q1S5 anopheles g
59	8	1.5	533	2	Q9SY99	Q9SY99 arabidopsis
60	8	1.5	544	2	Q7Q580	Q7Q580 anopheles g
61	8	1.5	550	2	Q8W033	Q8W033 arabidopsis
62	8	1.5	550	2	Q940H4	Q940H4 arabidopsis
63	8	1.5	558	2	Q8S058	Q8S058 oryza sativ
64	8	1.5	559	2	Q9VYG7	Q9VYG7 drosophila
65	8	1.5	560	2	Q6PCD0	Q6PCD0 homo sapien
66	8	1.5	560	2	Q9P2U7	Q9P2U7 homo sapien
67	8	1.5	560	2	Q62634	Q62634 rattus norv
68	8	1.5	576	2	Q6INC8	Q6INC8 xenopus lae
69	8	1.5	584	2	Q8AW47	Q8AW47 brachydanio
70	8	1.5	588	2	Q8K1Q1	Q8K1Q1 rattus norv
71	8	1.5	588	2	Q7TSF2	Q7TSF2 rattus norv
72	8	1.5	589	2	Q8NDX2	Q8NDX2 homo sapien
73	8	1.5	592	2	Q7Q3R3	Q7Q3R3 anopheles g
74	8	1.5	601	2	Q8BFU8	Q8BFU8 mus musculu
75	8	1.5	695	2	Q76HF4	Q76HF4 seriola qui
76	8	1.5	728	2	Q9U2E0	Q9U2E0 caenorhabdi
77	8	1.5	863	2	Q9ADL8	Q9ADL8 polyangium
78	8	1.5	872	2	Q7SX79	Q7SX79 brachydanio
79	8	1.5	887	2	Q6BCK3	Q6BCK3 fugu rubrip
80	8	1.5	888	2	Q6DEI2	Q6DEI2 brachydanio
81	8	1.5	888	2	Q7Z2S7	Q7Z2S7 brachydanio
82	8	1.5	897	2	Q7ZT42	Q7ZT42 brachydanio
83	8	1.5	911	2	Q6BCK4	Q6BCK4 fugu rubrip
84	8	1.5	912	2	Q7ZT45	Q7ZT45 seriola qui
85	8	1.5	935	2	Q7Q6T9	Q7Q6T9 anopheles g
86	8	1.5	940	2	Q7XTN8	Q7XTN8 oryza sativ
87	8	1.5	949	2	Q9SMA4	Q9SMA4 oryza sativ
88	8	1.5	953	2	Q9V701	Q9V701 drosophila
89	8	1.5	1349	2	Q9L096	Q9L096 streptomyce
90	8	1.5	2180	2	Q9VAS8	Q9VAS8 drosophila
91	8	1.5	4128	1	PRKD_MOUSE	P97313 mus musculu
92	7	1.3	39	2	Q33434	Q33434 equus burch
93	7	1.3	39	2	Q33435	Q33435 equus caball
94	7	1.3	39	2	Q34493	Q34493 equus quagg
95	7	1.3	50	2	Q6EAN8	Q6EAN8 sus scrofa
96	7	1.3	54	2	Q88MK7	Q88MK7 pseudomonas
97	7	1.3	68	2	Q6IG36	Q6IG36 drosophila
98	7	1.3	71	2	Q6H710	Q6H710 oryza sativ
99	7	1.3	73	1	CATZ_BOVIN	P05689 bos taurus
100	7	1.3	73	2	Q96PF5	Q96PF5 homo sapien
101	7	1.3	81	2	Q711Z3	Q711Z3 lactobacill
102	7	1.3	84	2	Q7U5U8	Q7U5U8 synechococc
103	7	1.3	95	1	KRPT_ANAPL	P08335 anas platyr
104	7	1.3	99	2	Q6UXF0	Q6UXF0 homo sapien

105	7	1.3	99	2	Q924W3	Q924W3 rattus norv	178	7	1.3	187	2	Q7ZYV4	Q7zyv4 odontesthes
106	7	1.3	102	2	Q9B219	Q9b219 branchiosto	179	7	1.3	188	2	Q7PWJ4	Q7pwj4 anopheles g
107	7	1.3	103	2	Q64QW1	Q64qw1 bacterioides	180	7	1.3	188	2	Q6ESW6	Q6esw6 myotis myst
108	7	1.3	104	1	VATF THEVO	Q97cq1 thermoplasm	181	7	1.3	191	1	PMVK HUMAN	Q51126 homo sapien
109	7	1.3	106	2	Q725U9	Q725u9 desulfovibr	182	7	1.3	191	1	PMVK_MOUSE	Q9d1g2 mus musculu
110	7	1.3	107	2	O13532	O13532 saccharomyc	183	7	1.3	192	2	Q8YFN3	Q8yfn3 brucella me
111	7	1.3	109	2	Q87TK8	Q87tk8 vibrio para	184	7	1.3	192	2	Q8G280	Q8g280 brucella su
112	7	1.3	114	2	Q32461	Q32461 actinomadur	185	7	1.3	193	2	Q8LW42	Q8lww2 coregonus l
113	7	1.3	115	2	Q37739	Q37739 felis silve	186	7	1.3	193	2	Q8MOM2	Q8m0m2 coregonus l
114	7	1.3	116	2	Q8HCW7	Q8hcv7 plecotus ma	187	7	1.3	193	2	Q8MOM3	Q8m0m3 coregonus l
115	7	1.3	116	2	Q94JE6	Q94je6 oryza sativ	188	7	1.3	193	2	Q8MOM4	Q8m0m4 coregonus l
116	7	1.3	118	2	Q64QD8	Q64qd8 bacterioides	189	7	1.3	193	2	Q8MOM5	Q8m0m5 coregonus l
117	7	1.3	118	2	Q8CRD8	Q8crd8 staphylococ	190	7	1.3	193	2	Q8MOM6	Q8m0m6 coregonus l
118	7	1.3	124	1	Q9T4W9	Q9t4w9 arabacia lix	191	7	1.3	193	2	Q8C4W2	Q8c4w2 mus musculu
119	7	1.3	125	1	NULM ARBLI	Q33756 arabacia lix	192	7	1.3	195	2	Q9Z8B8	Q9z8b8 chlamydia p
120	7	1.3	125	2	Q6M0T0	Q6m0t0 methanococc	193	7	1.3	195	2	Q8JM30	Q8jm30 mamestra co
121	7	1.3	126	1	ACPS_VIBCH	Q9kpb6 vibrio chol	194	7	1.3	195	2	Q8QLA9	Q8qla9 mamestra co
122	7	1.3	126	2	QYTH7	Q9yth7 caenorhabdi	195	7	1.3	195	2	Q7IA87	Q7ia87 mamestra co
123	7	1.3	127	2	Q3ER8	Q3er8 bacillus ce	196	7	1.3	195	2	Q8JIN3	Q8jin3 hippoglossu
124	7	1.3	129	1	PMVK_PIG	Q29081 sus scrofa	197	7	1.3	195	2	SOMA_FUGRU	O12980 fugu rubrip
125	7	1.3	129	2	Q8QNH2	Q8qnh2 ectocarpus	198	7	1.3	196	1	SOMA_SIGGU	Q9ibes5 siganus gut
126	7	1.3	131	2	Q7QXE3	Q7qxe3 giardia lam	199	7	1.3	196	2	Q823F1	Q823p1 chlamyidophi
127	7	1.3	132	2	Q8TVH5	Q8tvh5 methanopyru	200	7	1.3	197	1	Y089_MYCTU	P65346 mycobacteri
128	7	1.3	133	2	Q9Y928	Q9y928 acroporum p	201	7	1.3	197	1	Y092_MYCBO	P65347 mycobacteri
129	7	1.3	135	2	Q8W128	Q8w128 capsicum ex	202	7	1.3	199	2	Q6MKU1	Q6mkul bdellovibri
130	7	1.3	136	2	Q8W128	Q8w128 capsicum ex	203	7	1.3	200	2	Q8NGA3	Q8nga3 homo sapien
131	7	1.3	138	1	YCM2_SCHPO	Q94249 schizosacch	204	7	1.3	200	2	O79237	O79237 thymallus a
132	7	1.3	142	2	Q7X8R7	Q7x8r7 oxyza sativ	205	7	1.3	200	2	Q9T4G7	Q9t4g7 thymallus a
133	7	1.3	143	2	Q91I70	Q91i70 helicoverpa	206	7	1.3	200	2	Q892Y5	Q892y5 clostroidum
134	7	1.3	146	2	Q7NGX7	Q7ngx7 gloebacter	207	7	1.3	201	2	Q8JZR7	Q8jzr7 mus musculu
135	7	1.3	148	2	Q9ITJ4	Q9itj4 tupaiid her	208	7	1.3	202	2	Q9NTR6	Q9ntr6 homo sapien
136	7	1.3	150	2	Q94WB2	Q94wb2 ptereleotri	209	7	1.3	202	2	Q9V8V0	Q9v8v0 drosophila
137	7	1.3	150	2	Q94WD3	Q94wd3 ptereleotri	210	7	1.3	202	2	Q9FHR1	Q9fhr1 arabidopsis
138	7	1.3	151	2	Q7PI79	Q7pi79 anopheles g	211	7	1.3	203	1	SOMA_PAGMA	P08591 pagrus majo
139	7	1.3	151	2	Q48800	Q48800 legionella	212	7	1.3	203	1	SOMA_VERVA	Q93566 verasper va
140	7	1.3	151	2	Q6QF8	Q6qff8 legionella	213	7	1.3	203	2	Q7MQW7	Q7mqw7 wolinnella s
141	7	1.3	151	2	Q6QF8	Q6qff8 legionella	214	7	1.3	203	2	Q8JIN5	Q8jin5 cottus kazi
142	7	1.3	151	2	Q6QF3	Q6qfg3 legionella	215	7	1.3	204	1	SOMA_AACABU	Q01282 acanthopagr
143	7	1.3	151	2	Q6QFH0	Q6qfh0 legionella	216	7	1.3	204	1	SOMA_ACALA	P45654 acanthopagr
144	7	1.3	152	2	Q02116	Q02116 rhizopus st	217	7	1.3	204	1	SOMA_DICLA	Q05163 dicentrarch
145	7	1.3	153	2	Q8KUY1	Q8kuy1 vibrio chol	218	7	1.3	204	1	SOMA_LATCA	Q01283 lates calca
146	7	1.3	154	2	Q7S1E3	Q7sie3 neurospora	219	7	1.3	204	1	SOMA_MORSA	P48248 morone saxa
147	7	1.3	155	2	Q8W129	Q8w129 capsicum ca	220	7	1.3	204	1	SOMA_ODOAR	Q91915 odontesthes
148	7	1.3	155	2	Q41459	Q41459 seriola qui	221	7	1.3	204	1	SOMA_OREMO	P34746 oreochromis
149	7	1.3	158	2	Q9CCU7	Q9ccu7 mycobacteri	222	7	1.3	204	1	SOMA_ORENI	P13391 oreochromis
150	7	1.3	160	2	Q9CSW6	Q9csw6 mus musculu	223	7	1.3	204	1	SOMA_PBRFV	Q9d393 perca flave
151	7	1.3	161	2	Q6GKY2	Q6gky2 arabidopsis	224	7	1.3	204	1	SOMA_PSECR	Q9194 pseudosciae
152	7	1.3	165	2	Q8UDC2	Q8udc2 agrobacteri	225	7	1.3	204	1	SOMA_SCIOC	Q91b1l sciaenops o
153	7	1.3	166	2	Q8LXA6	Q8lxa6 debaryomyce	226	7	1.3	204	1	SOMA_SEBSC	P87391 sebaestes sc
154	7	1.3	168	2	Q9UTU7	Q9utu7 schizosacch	227	7	1.3	204	1	SOMA_SERQU	P09539 seriola qui
155	7	1.3	168	2	Q7U595	Q7u595 synechococc	228	7	1.3	204	1	SOMA_SPAAU	P29971 sparus aura
156	7	1.3	169	2	O07698	O07698 mycobacteri	229	7	1.3	204	1	SOMA_THUTH	P09113 thunnus thy
157	7	1.3	171	2	Q837C3	Q837c3 enterococcu	230	7	1.3	204	1	SOMA_TRITC	Q98uf6 trichogaste
158	7	1.3	171	2	Q9KYH0	Q9kyh0 streptomyce	231	7	1.3	204	2	Q8UW02	Q8uw02 epinephelus
159	7	1.3	173	2	Q82HK8	Q82hk8 streptomyce	232	7	1.3	204	2	Q90VV6	Q90vv6 epinephelus
160	7	1.3	176	2	Q9RPS9	Q9rps9 enterococcu	233	7	1.3	204	2	Q90YK4	Q90yk4 sparus aura
161	7	1.3	176	2	Q6N353	Q6n353 rhodopsendo	234	7	1.3	204	2	O6LAL0	O6lala0 oreochromis
162	7	1.3	179	2	Q7NH52	Q7nh52 gloeobacter	235	7	1.3	204	2	O6QRJ2	O6qlr2 leporinis cya
163	7	1.3	181	2	Q88ZC1	Q88zc1 lactobacill	236	7	1.3	204	2	Q7SYG9	O7syg9 siniperca k
164	7	1.3	182	2	Q8EGY7	Q8egy7 plecotus au	237	7	1.3	204	2	Q7TIG3	Q7tig3 epinephelus
165	7	1.3	182	2	Q6EGY8	Q6egy8 plecotus au	238	7	1.3	204	2	Q7T231	Q7t231 monopteris
166	7	1.3	182	2	Q6EGY9	Q6egy9 plecotus ma	239	7	1.3	208	2	Q8STK6	Q8stk6 encephalito
167	7	1.3	182	2	Q6EGZ0	Q6egz0 plecotus ma	240	7	1.3	210	2	Q9RCV9	Q9rcv9 streptomyce
168	7	1.3	182	2	Q6EGZ1	Q6egz1 plecotus au	241	7	1.3	210	2	Q9CXB8	Q9cxb8 mus musculu
169	7	1.3	182	2	Q84455	Q84455 paramecium	242	7	1.3	211	2	Q943X3	Q943x3 oryza sativ
170	7	1.3	185	1	SOMA_KATPE	P20391 katsuonus	243	7	1.3	211	2	Q7N6C9	Q7n6c9 photohabdu
171	7	1.3	185	2	Q89NE1	Q89ne1 bradyrhizob	244	7	1.3	213	2	Q8WB47	Q8wb47 bufo macula
172	7	1.3	185	2	Q6UAM5	Q6uam5 tetraodon n	245	7	1.3	213	2	O6VZK8	O6vzk8 canarypox v
173	7	1.3	186	2	O85609	O85609 escherichia	246	7	1.3	215	2	Q8RTT8	Q8rtt8 uncultured
174	7	1.3	187	1	SOMA_THUAL	P34747 thunnus alb	247	7	1.3	215	2	O6SPD5	O6spf5 unclutred
175	7	1.3	187	2	Q91077	Q91077 lsteolabrax	248	7	1.3	217	1	ATOD_HAEIN	P44875 haemophilus
176	7	1.3	187	2	Q91449	Q91449 seriola dum	249	7	1.3	217	1	OPBB_BACSU	Q45461 bacillus su
177	7	1.3	187	2	Q91454	Q91454 sebaestiscus	250	7	1.3	217	1	OPCB_BACSU	O34878 bacillus su

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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:34:43 ; Search time 27.0339 seconds
(without alignments)
1907.682 Million cell updates/sec

Title: US-09-776-865-2
Perfect score: 536
Sequence: 1 MACAGMTTPRPVQPARPGF.....LFAKGEVQNALNDHGHHRH 536

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	2.1	465	2 139473	Na+-dependent phos
2	11	2.1	467	2 A48916	sodium phosphate t
3	10	1.9	544	2 T24633	hypothetical prote
4	10	1.9	573	2 T23589	hypothetical prote
5	9	1.7	465	2 S59915	sodium-phosphate t
6	9	1.7	715	2 H71352	probable sigma fac
7	8	1.5	250	2 A56572	homeotic protein H
8	8	1.5	308	2 AG0992	high-affinity bran
9	8	1.5	308	2 JH0668	high-affinity bran
10	8	1.5	373	2 C70806	probable fadE27 pr
11	8	1.5	396	2 T23619	hypothetical prote
12	8	1.5	398	2 G71733	hypothetical prote
13	8	1.5	465	2 A56410	sodium/phosphate t
14	8	1.5	479	2 E69613	ATP-dependent RNA
15	8	1.5	533	2 T04770	aldehyde dehydroge
16	8	1.5	560	2 I59302	brain specific Na+
17	8	1.5	4128	2 JC6306	protein kinase (EC
18	7	1.3	33	2 S13863	dihydrolipoamide d
19	7	1.3	73	2 A29172	cathepsin B-like c
20	7	1.3	95	1 KRDKF4	keratin B-4, feath
21	7	1.3	107	2 S69295	probable membrane
22	7	1.3	114	2 JC5860	polyketide synthas
23	7	1.3	126	2 F82072	holo-(acyl-carrier
24	7	1.3	133	2 H72476	hypothetical prote
25	7	1.3	138	2 T40963	very hypothetical
26	7	1.3	151	2 S61384	icmW protein - leg
27	7	1.3	152	2 PT0433	progesterone 11alp
28	7	1.3	153	2 E82330	conserved hypothet
29	7	1.3	158	2 C86961	probable tRNA/tRNA

30	7	1.3	165	2 C97624	petP protein (impo
31	7	1.3	165	2 AD2847	transcription regu
32	7	1.3	182	2 T17625	hypothetical prote
33	7	1.3	185	2 JK0021	somatotropin - ski
34	7	1.3	187	2 A61123	somatotropin - Moz
35	7	1.3	187	2 PC1082	somatotropin - Jap
36	7	1.3	187	2 JU0030	somatotropin - yel
37	7	1.3	187	2 PC1087	somatotropin - dus
38	7	1.3	187	2 PC1088	somatotropin - gre
39	7	1.3	192	2 AI3437	colicin v producti
40	7	1.3	195	2 G86543	CR276 hypothetical
41	7	1.3	195	2 C72081	conserved hypothet
42	7	1.3	197	2 A70750	hypothetical prote
43	7	1.3	203	2 S00747	somatotropin precu
44	7	1.3	204	1 STFI	somatotropin precu
45	7	1.3	204	2 A56642	somatotropin precu
46	7	1.3	204	2 I51289	somatotropin - Mor
47	7	1.3	204	2 JN0484	somatotropin precu
48	7	1.3	204	2 JH0577	somatotropin precu
49	7	1.3	204	2 A56904	somatotropin precu
50	7	1.3	204	2 S30451	somatotropin - Aca
51	7	1.3	204	2 JC4261	somatotropin precu
52	7	1.3	204	2 S01746	somatotropin precu
53	7	1.3	217	2 B64092	butyrate-acetoacet
54	7	1.3	217	2 D69670	glycine betaine/ca
55	7	1.3	217	2 H69669	choline ABC transp
56	7	1.3	218	2 A95295	probable ABC trans
57	7	1.3	225	2 B83083	conserved hypothet
58	7	1.3	232	2 AF3406	hypothetical expor
59	7	1.3	233	2 A69004	CDPdiacylglycerol-
60	7	1.3	236	2 S42069	TSGT protein - rat
61	7	1.3	241	2 D87547	3-oxoadipate CoA-t
62	7	1.3	242	2 AE2314	ATP-binding protei
63	7	1.3	249	2 A99667	hypothetical prote
64	7	1.3	251	2 T47109	3-oxoadipate CoA-t
65	7	1.3	251	2 F72114	conserved hypothet
66	7	1.3	251	2 A86508	ACR family import
67	7	1.3	260	2 T35021	probable 3-oxoadip
68	7	1.3	279	2 E64109	dimethylsulfoxide
69	7	1.3	282	2 E95128	conserved hypothet
70	7	1.3	282	2 E97999	conserved hypothet
71	7	1.3	284	2 C70165	inositol monophosp
72	7	1.3	285	2 S08491	hypothetical prote
73	7	1.3	285	2 S74771	hypothetical prote
74	7	1.3	288	2 D85072	hypothetical prote
75	7	1.3	298	2 E97032	probable permease
76	7	1.3	299	2 E85517	probable LysR-like
77	7	1.3	300	2 AE0762	conserved hypothet
78	7	1.3	301	2 C75447	conserved hypothet
79	7	1.3	304	2 H75081	phosphate abc tran
80	7	1.3	305	1 H75285	probable phosphoes
81	7	1.3	307	2 E91206	probable ARAC-type
82	7	1.3	307	2 G86052	probable ARAC-type
83	7	1.3	307	2 A65170	hypothetical prote
84	7	1.3	307	2 AH3112	hypothetical prote
85	7	1.3	307	2 E98174	oligopeptide ABC t
86	7	1.3	313	2 B71390	NADH2 dehydrogenas
87	7	1.3	315	2 E64426	NADH2 dehydrogenas
88	7	1.3	317	2 T11337	NADH2 dehydrogenas
89	7	1.3	318	1 QXBQIM	NADH2 dehydrogenas
90	7	1.3	318	2 A58888	NADH2 dehydrogenas
91	7	1.3	318	2 S47870	NADH2 dehydrogenas
92	7	1.3	318	2 T11428	NADH2 dehydrogenas
93	7	1.3	318	2 T11441	NADH2 dehydrogenas
94	7	1.3	318	2 T11440	NADH2 dehydrogenas
95	7	1.3	318	2 T11493	NADH2 dehydrogenas
96	7	1.3	318	2 T11402	NADH2 dehydrogenas
97	7	1.3	318	2 S41835	NADH2 dehydrogenas
98	7	1.3	318	2 S26151	NADH2 dehydrogenas
99	7	1.3	318	2 A58850	NADH2 dehydrogenas
100	7	1.3	318	2 S41820	NADH2 dehydrogenas
101	7	1.3	318	2 T45550	NADH2 dehydrogenas
102	7	1.3	318	2 T11363	NADH2 dehydrogenas

103	7	1.3	318	2	T11857	NADH2 dehydrogenas	176	7	1.3	528	2	G90569	hypothetical prote
104	7	1.3	318	2	T11247	NADH2 dehydrogenas	177	7	1.3	533	2	S10841	gene ND5 intron 1
105	7	1.3	318	2	T10972	NADH2 dehydrogenas	178	7	1.3	535	2	T03260	cytochrome P450 -
106	7	1.3	318	2	T11050	NADH2 dehydrogenas	179	7	1.3	535	2	T03246	cytochrome P450 -
107	7	1.3	321	2	T13811	NADH2 dehydrogenas	180	7	1.3	535	2	JC7858	GroEL protein - Te
108	7	1.3	321	2	S55004	NADH2 dehydrogenas	181	7	1.3	540	2	H98086	chaperonin GroEL [
109	7	1.3	321	2	AS0775	probable sugar kin	182	7	1.3	540	2	G95222	chaperonin, 60 kDa
110	7	1.3	322	2	S68128	NADH2 dehydrogenas	183	7	1.3	541	2	S72614	chaperonin, 60 kDa
111	7	1.3	323	1	QXKL1M	NADH2 dehydrogenas	184	7	1.3	542	1	A70220	phosphotransferase
112	7	1.3	323	2	T11793	NADH2 dehydrogenas	185	7	1.3	544	2	JC6063	chaperonin groEL -
113	7	1.3	323	2	A34284	NADH2 dehydrogenas	186	7	1.3	544	2	B41884	58K heat shock pro
114	7	1.3	323	2	AS8892	NADH2 dehydrogenas	187	7	1.3	544	2	JC5130	heat shock protein
115	7	1.3	323	2	T09857	NADH2 dehydrogenas	188	7	1.3	544	2	B83720	class I heat-shock
116	7	1.3	323	2	T11820	NADH2 dehydrogenas	189	7	1.3	545	2	S10842	gene ND5 intron 2
117	7	1.3	323	2	T12486	hypothetical prote	190	7	1.3	558	2	G87450	conserved hypothet
118	7	1.3	324	2	S36002	NADH2 dehydrogenas	191	7	1.3	559	2	S62503	inorganic phosphat
119	7	1.3	324	2	S35462	NADH2 dehydrogenas	192	7	1.3	561	2	T49979	cytochrome P450-li
120	7	1.3	324	2	T09947	NADH2 dehydrogenas	193	7	1.3	563	2	T43650	probable sodium-de
121	7	1.3	324	2	C41608	hypothetical prote	194	7	1.3	568	2	AG2264	urease alpha chain
122	7	1.3	325	2	H86670	hypothetical prote	195	7	1.3	570	2	T49181	cyclophillin-like p
123	7	1.3	326	2	H71884	iron (III) dicitrat	196	7	1.3	576	2	H88548	protein ZK512.6 [i
124	7	1.3	326	2	A64631	iron(III) dicitrat	197	7	1.3	580	2	T39122	amino-acid permeas
125	7	1.3	334	2	T46885	3-methyl-2-oxobuta	198	7	1.3	594	2	T38114	pyruvate decarboxy
126	7	1.3	334	2	T36511	probable branched-	199	7	1.3	600	2	E48951	nisin transport pr
127	7	1.3	336	2	C86921	conserved hypothet	200	7	1.3	605	2	T43191	probable pyruvate
128	7	1.3	333	2	T14245	NADH2 dehydrogenas	201	7	1.3	663	2	T38155	78 kd glucose regu
129	7	1.3	353	2	G02729	thrombopoietin - h	202	7	1.3	663	2	S20877	dnak-type molecula
130	7	1.3	353	2	I80105	thrombopoietin pre	203	7	1.3	674	2	I55476	growth potentiatin
131	7	1.3	359	2	T39944	hypothetical trans	204	7	1.3	678	2	B48089	growth arrest-spec
132	7	1.3	365	2	S50610	hypothetical prote	205	7	1.3	687	2	S74621	carbon dioxide con
133	7	1.3	370	2	AS0602	probable membrane	206	7	1.3	706	2	G90696	hypothetical prote
134	7	1.3	380	2	T29248	hypothetical prote	207	7	1.3	715	2	S10843	NADH2 dehydrogenas
135	7	1.3	384	2	A70805	probable lprN prot	208	7	1.3	720	2	C85547	probable cytoplasm
136	7	1.3	390	2	T50037	capsular polysacch	209	7	1.3	734	2	H86340	sugar transporter
137	7	1.3	392	2	JC7633	aryl hydrocarbon n	210	7	1.3	734	2	T51139	sugar transport pr
138	7	1.3	405	2	E89977	conserved hypothet	211	7	1.3	752	2	G02273	liv-1 protein - hu
139	7	1.3	407	2	F70696	hypothetical prote	212	7	1.3	753	2	T46614	chemotaxis protein
140	7	1.3	422	2	C82912	phosphoglycerate k	213	7	1.3	765	2	A69440	conserved hypothet
141	7	1.3	422	2	S73667	adhesin p1 precurs	214	7	1.3	778	2	T17679	proline-rich prote
142	7	1.3	423	2	T04915	CPD-diacylglycerol	215	7	1.3	781	2	T02272	hypothetical prote
143	7	1.3	423	2	G85255	CPD-diacylglycerol	216	7	1.3	792	2	S32244	X-Pro dipeptidyl-p
144	7	1.3	424	2	T07366	probable phosphati	217	7	1.3	796	2	T20393	hypothetical prote
145	7	1.3	427	2	T01455	CPD-diacylglycerol	218	7	1.3	803	2	B84931	DNA topoisomerase
146	7	1.3	428	2	S03767	cellulase (EC 3.2.	219	7	1.3	837	2	T12514	hypothetical prote
147	7	1.3	428	2	S73379	adhesin p1 precurs	220	7	1.3	847	2	G65370	cation-transportin
148	7	1.3	438	2	T04800	CPD-diacylglycerol	221	7	1.3	877	2	S75207	alpha-glucosidase
149	7	1.3	438	2	S73952	adhesin p1 precurs	222	7	1.3	924	2	S75284	chemotaxis protein
150	7	1.3	443	2	AD3050	MFS permease [alph	223	7	1.3	925	2	B83529	sensor/response re
151	7	1.3	443	2	S77166	hypothetical prote	224	7	1.3	1005	1	P1VXPJ	RNA 1 protein - pe
152	7	1.3	451	2	G69392	multidrug resistan	225	7	1.3	1085	2	F96712	hypothetical prote
153	7	1.3	458	2	T49004	transporter-like p	226	7	1.3	1144	2	T20218	hypothetical prote
154	7	1.3	459	2	F84935	argininosuccinate	227	7	1.3	1189	2	T51491	hypothetical prote
155	7	1.3	460	2	AD0968	sodium,galactoside	228	7	1.3	1275	2	B28096	line-1 protein ORF
156	7	1.3	461	2	D84971	phosphotransferase	229	7	1.3	1275	2	I38588	reverse transcript
157	7	1.3	461	2	G85059	probable sugar tra	230	7	1.3	1275	2	S65824	reverse transcript
158	7	1.3	462	2	B32840	anthranilate synth	231	7	1.3	1323	2	T18214	ATP binding casset
159	7	1.3	472	2	S28286	hypothetical prote	232	7	1.3	1627	1	IJYMAP	adhesin p1 precurs
160	7	1.3	473	2	S20612	triacylglycerol li	233	7	1.3	1635	2	A41480	adhesin p1, group
161	7	1.3	477	2	H83588	probable MFS trans	234	7	1.3	1682	2	A45380	sodium channel pro
162	7	1.3	477	2	H98235	probable mfs dicar	235	7	1.3	1683	2	T30885	complement compone
163	7	1.3	479	2	S31195	probable permease	236	7	1.3	1969	2	T08875	histidine kinase h
164	7	1.3	479	2	F86042	probable permease	237	7	1.3	2130	2	AB0821	probable exported
165	7	1.3	479	2	C65167	hypothetical 51.0	238	7	1.3	2145	2	S61041	glutamate synthase
166	7	1.3	487	2	G95315	probable [imported	239	7	1.3	2649	2	T51023	hypothetical prote
167	7	1.3	493	2	AE3077	aldehyde dehydroge	240	7	1.3	2890	2	B71846	dna-directed RNA p
168	7	1.3	493	2	D82099	aldehyde dehydroge	241	7	1.3	2890	2	F64669	DNA-directed RNA p
169	7	1.3	493	2	G88553	protein C38C10.2 [242	7	1.3	3122	2	T17202	DNA-directed DNA p
170	7	1.3	500	1	E69291	4-hydroxyphenylace	243	6	1.1	10	2	B60589	sperm-activating p
171	7	1.3	500	2	T49978	cytochrome P450-li	244	6	1.1	13	2	D61491	seed protein ws-4
172	7	1.3	504	2	T34411	hypothetical prote	245	6	1.1	18	2	A41877	LcrKc - Yersinia p
173	7	1.3	515	2	E71447	probable PSII D1 p	246	6	1.1	22	2	JP0069	ribosomal protein
174	7	1.3	517	2	A48250	U2AF-homologous pr	247	6	1.1	25	2	A60704	serine proteinase
175	7	1.3	523	2	S50479	26S proteasome reg	248	6	1.1	25	2	JP0067	ribosomal protein

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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:55:49 ; Search time 115.414 Seconds
(without alignment)

1794.174 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 536

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1726216 seqs, 386330316 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	536	100.0	536	9 US-09-776-865-2	Sequence 2, Appli
2	536	100.0	536	17 US-10-823-506-8	Sequence 8, Appli
3	495	92.4	495	9 US-09-915-181A-7	Sequence 7, Appli
4	495	92.4	495	16 US-10-755-889-588	Sequence 588, App
5	495	92.4	495	17 US-10-823-506-2	Sequence 2, Appli
6	284	53.0	284	15 US-10-264-049-2477	Sequence 2477, Ap
7	217	40.5	272	15 US-10-264-237-2351	Sequence 1200, Ap
8	180	33.6	194	15 US-10-296-115-1200	Sequence 4, Appli
9	61	11.4	495	9 US-09-776-865-4	Sequence 4, Appli
10	61	11.4	495	17 US-10-823-506-4	Sequence 4, Appli
11	14	2.6	495	17 US-10-823-506-10	Sequence 10, Appli

12	14	2.6	495	17	US-10-823-506-12	Sequence 12, Appli
13	11	2.1	467	9	US-09-991-212A-3	Sequence 3, Appli
14	11	2.1	467	10	US-09-965-522-3	Sequence 3, Appli
15	11	2.1	467	17	US-10-877-818-3	Sequence 3, Appli
16	11	2.1	578	9	US-09-740-041-4	Sequence 4, Appli
17	11	2.1	578	14	US-10-389-967-4	Sequence 4, Appli
18	11	2.1	582	9	US-09-915-181A-4	Sequence 4, Appli
19	11	2.1	582	15	US-10-205-331-7	Sequence 7, Appli
20	11	2.1	582	16	US-10-734-731-10	Sequence 10, Appli
21	11	2.1	582	16	US-10-734-731-12	Sequence 12, Appli
22	11	2.1	582	16	US-10-734-731-14	Sequence 14, Appli
23	11	2.1	582	16	US-10-807-500-10	Sequence 10, Appli
24	11	2.1	582	16	US-10-807-500-12	Sequence 12, Appli
25	11	2.1	582	16	US-10-807-500-14	Sequence 14, Appli
26	10	1.9	544	15	US-10-369-493-5873	Sequence 5873, Ap
27	10	1.9	573	15	US-10-369-493-5871	Sequence 5871, Ap
28	10	1.9	573	15	US-10-369-493-5872	Sequence 5872, Ap
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30	8	1.5	71	16	US-10-425-115-288336	Sequence 288336,
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32	8	1.5	114	16	US-10-437-963-128557	Sequence 128557,
33	8	1.5	143	16	US-10-425-115-335986	Sequence 335986,
34	8	1.5	154	16	US-10-767-701-52130	Sequence 52130, A
35	8	1.5	232	15	US-10-425-114-43907	Sequence 43907, A
36	8	1.5	235	15	US-10-282-122A-56379	Sequence 56379, A
37	8	1.5	264	15	US-10-108-260A-3281	Sequence 3281, Ap
38	8	1.5	373	16	US-10-482-706-253	Sequence 253, App
39	8	1.5	384	15	US-10-424-599-183068	Sequence 183068,
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41	8	1.5	479	15	US-10-369-493-23364	Sequence 23364, A
42	8	1.5	512	16	US-10-425-115-335979	Sequence 335979,
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44	8	1.5	560	9	US-09-991-212A-4	Sequence 4, Appli
45	8	1.5	560	10	US-09-965-522-4	Sequence 5, Appli
46	8	1.5	560	15	US-10-314-790-5	Sequence 4, Appli
47	8	1.5	560	16	US-10-734-731-2	Sequence 2, Appli
48	8	1.5	560	16	US-10-734-731-4	Sequence 4, Appli
49	8	1.5	560	16	US-10-734-731-6	Sequence 6, Appli
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62	8	1.5	601	18	US-10-499-731-46	Sequence 46, Appli
63	8	1.5	850	9	US-09-915-181A-3	Sequence 3, Appli
64	8	1.5	940	16	US-10-437-963-155833	Sequence 155833,
65	8	1.5	949	17	US-10-732-923-18652	Sequence 18652, A
66	8	1.5	950	16	US-10-437-963-107881	Sequence 107881,
67	8	1.5	1031	16	US-10-437-963-107870	Sequence 107870,
68	8	1.5	4128	14	US-10-205-194-1	Sequence 1, Appli
69	7	1.3	13	15	US-10-469-101-69	Sequence 69, Appli
70	7	1.3	13	15	US-10-469-101-70	Sequence 70, Appli
71	7	1.3	13	15	US-10-469-101-71	Sequence 71, Appli
72	7	1.3	13	14	US-10-191-879-31	Sequence 31, Appli
73	7	1.3	33	10	US-09-983-802-663	Sequence 663, App
74	7	1.3	33	10	US-09-984-490-663	Sequence 663, App
75	7	1.3	33	11	US-09-973-278-444	Sequence 444, App
76	7	1.3	42	15	US-10-424-599-212978	Sequence 212978,
77	7	1.3	44	10	US-09-895-298-126	Sequence 126, App
78	7	1.3	44	16	US-10-885-039-126	Sequence 320119,
79	7	1.3	58	16	US-10-425-115-350119	Sequence 204921,
80	7	1.3	59	16	US-10-437-963-204921	Sequence 218670,
81	7	1.3	61	15	US-10-424-599-218670	Sequence 180080,
82	7	1.3	64	15	US-10-424-599-180080	Sequence 149839,
83	7	1.3	65	15	US-10-424-599-149839	Sequence 147591,
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85	7	1.3	71	16	US-10-425-115-254514	Sequence 254514,	158	7	1.3	204	14	US-10-191-879-6	Sequence 6, Appli
86	7	1.3	71	16	US-10-425-115-318386	Sequence 318386,	159	7	1.3	204	15	US-10-104-047-2253	Sequence 2253, Ap
87	7	1.3	72	16	US-10-437-963-181072	Sequence 181072,	160	7	1.3	206	9	US-09-925-298-538	Sequence 538, App
88	7	1.3	76	15	US-10-424-599-255605	Sequence 255605,	161	7	1.3	206	14	US-10-102-806-538	Sequence 538, App
89	7	1.3	77	15	US-10-424-599-168281	Sequence 168281,	162	7	1.3	206	16	US-10-767-701-32217	Sequence 32217, A
90	7	1.3	78	16	US-10-425-115-357514	Sequence 357514,	163	7	1.3	207	15	US-10-264-237-1787	Sequence 1787, Ap
91	7	1.3	79	10	US-09-764-891-4448	Sequence 4448, A	164	7	1.3	212	15	US-10-424-599-160649	Sequence 160649,
92	7	1.3	82	9	US-09-864-761-35759	Sequence 35759, Ap	165	7	1.3	214	16	US-10-767-701-34424	Sequence 34424, A
93	7	1.3	85	16	US-10-437-963-188238	Sequence 188238,	166	7	1.3	223	9	US-09-925-300-1346	Sequence 1346, Ap
94	7	1.3	87	15	US-10-424-599-148365	Sequence 148365,	167	7	1.3	223	15	US-10-432-290-38	Sequence 38, Appl
95	7	1.3	88	16	US-10-425-115-253274	Sequence 253274,	168	7	1.3	223	18	US-10-276-7798-1	Sequence 1, Appli
96	7	1.3	91	16	US-10-425-115-310462	Sequence 310462,	169	7	1.3	228	15	US-10-432-290-24	Sequence 24, Appl
97	7	1.3	96	15	US-10-424-599-243646	Sequence 243646,	170	7	1.3	232	16	US-10-437-963-103966	Sequence 103966,
98	7	1.3	97	16	US-10-437-963-110377	Sequence 110377,	171	7	1.3	233	15	US-10-424-599-198853	Sequence 198853,
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100	7	1.3	98	16	US-10-437-963-161222	Sequence 161222,	173	7	1.3	251	15	US-10-312-273-141	Sequence 141, App
101	7	1.3	101	15	US-10-424-599-199724	Sequence 199724,	174	7	1.3	251	15	US-10-289-762-156	Sequence 156, App
102	7	1.3	103	15	US-10-094-749-2113	Sequence 2113, Ap	175	7	1.3	252	15	US-10-424-599-180645	Sequence 180645,
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106	7	1.3	106	14	US-10-083-357-972	Sequence 972, App	179	7	1.3	260	14	US-10-156-761-9239	Sequence 9239, Ap
107	7	1.3	108	16	US-10-425-115-253034	Sequence 253034,	180	7	1.3	268	16	US-10-425-115-319762	Sequence 319762,
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111	7	1.3	116	16	US-10-437-963-108779	Sequence 108779,	184	7	1.3	282	16	US-10-472-928-2212	Sequence 2212, Ap
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114	7	1.3	122	14	US-10-312-187-12	Sequence 12, Appl	187	7	1.3	292	16	US-10-322-281-494	Sequence 494, App
115	7	1.3	125	16	US-10-425-115-332340	Sequence 332340,	188	7	1.3	295	10	US-09-813-153-128	Sequence 128, App
116	7	1.3	126	15	US-10-282-122A-77481	Sequence 77481, A	189	7	1.3	302	17	US-10-659-004-104	Sequence 104, App
117	7	1.3	127	15	US-10-424-599-160647	Sequence 160647,	190	7	1.3	303	15	US-10-369-386-5	Sequence 5, Appli
118	7	1.3	129	16	US-10-767-701-39962	Sequence 39962, A	191	7	1.3	303	15	US-10-390-191-2	Sequence 2, Appli
119	7	1.3	133	16	US-10-767-701-49108	Sequence 49108, A	192	7	1.3	303	16	US-10-723-860-4548	Sequence 4548, Ap
120	7	1.3	135	10	US-09-764-891-4759	Sequence 4759, Ap	193	7	1.3	304	15	US-10-108-260A-4214	Sequence 4214, Ap
121	7	1.3	142	16	US-10-437-963-174382	Sequence 174382,	194	7	1.3	306	15	US-10-393-840-937	Sequence 937, App
122	7	1.3	143	15	US-10-424-599-213589	Sequence 213589,	195	7	1.3	307	14	US-10-304-928-16	Sequence 16, Appl
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Title: US-09-776-865-2

Perfect score: 536

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Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

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145	7	1.3	512	4	US-09-902-540-15789	Sequence 15789, A	218	6	1.1	42	4	US-09-399-003-41	Sequence 41, Appli
146	7	1.3	523	4	US-09-538-092-234	Sequence 234, App	219	6	1.1	43	4	US-09-489-847-225	Sequence 225, App
147	7	1.3	540	4	US-09-252-991A-22555	Sequence 22555, A	220	6	1.1	44	4	US-09-205-258-257	Sequence 257, App
148	7	1.3	540	4	US-09-583-110-3685	Sequence 3685, Ap	221	6	1.1	50	3	US-09-282-856A-1	Sequence 1, Appli
149	7	1.3	552	4	US-09-270-767-45540	Sequence 45540, A	222	6	1.1	51	4	US-09-270-767-57646	Sequence 57646, A
150	7	1.3	563	4	US-09-915-181A-6	Sequence 6, Appli	223	6	1.1	52	4	US-09-621-976-6359	Sequence 6359, Ap
151	7	1.3	574	4	US-09-248-796A-16849	Sequence 16849, A	224	6	1.1	54	4	US-09-270-767-57137	Sequence 57137, A
152	7	1.3	576	3	US-08-864-785-1	Sequence 1, Appli	225	6	1.1	56	3	US-09-177-249-166	Sequence 166, App
153	7	1.3	641	4	US-09-613-303-51	Sequence 51, Appli	226	6	1.1	56	4	US-09-755-665-53	Sequence 53, Appli
154	7	1.3	641	4	US-10-267-311-51	Sequence 51, Appli	227	6	1.1	56	4	US-09-812-283-166	Sequence 166, App
155	7	1.3	663	1	US-08-441-139-7	Sequence 7, Appli	228	6	1.1	59	4	US-09-270-767-41846	Sequence 41846, A
156	7	1.3	678	1	US-08-282-141-2	Sequence 2, Appli	229	6	1.1	59	4	US-09-270-767-57088	Sequence 57088, A
157	7	1.3	678	1	US-08-435-434-2	Sequence 2, Appli	230	6	1.1	61	1	US-08-095-898-6	Sequence 6, Appli
158	7	1.3	678	1	US-08-435-436-2	Sequence 2, Appli	231	6	1.1	61	4	US-09-270-767-60545	Sequence 60545, A
159	7	1.3	678	2	US-08-438-863-2	Sequence 2, Appli	232	6	1.1	61	5	PCT-US92-09439-6	Sequence 6, Appli
160	7	1.3	678	2	US-08-438-864-2	Sequence 2, Appli	233	6	1.1	62	4	US-09-661-322A-26	Sequence 26, Appli
161	7	1.3	678	3	US-08-438-862-2	Sequence 2, Appli	234	6	1.1	62	4	US-09-270-767-59377	Sequence 59377, A
162	7	1.3	678	3	US-08-628-747-2	Sequence 2, Appli	235	6	1.1	62	4	US-09-248-796A-25193	Sequence 25193, A
163	7	1.3	678	3	US-08-402-253-2	Sequence 2, Appli	236	6	1.1	64	4	US-09-661-322A-32	Sequence 32, Appli
164	7	1.3	678	3	US-08-443-866B-2	Sequence 2, Appli	237	6	1.1	64	4	US-09-248-796A-26590	Sequence 26590, A
165	7	1.3	693	4	US-09-252-991A-20348	Sequence 20348, A	238	6	1.1	66	4	US-09-489-039A-11065	Sequence 11065, A
166	7	1.3	697	4	US-09-252-991A-21106	Sequence 21106, A	239	6	1.1	66	4	US-09-673-395A-165	Sequence 165, App
167	7	1.3	722	4	US-09-252-991A-26839	Sequence 26839, A	240	6	1.1	66	4	US-09-513-999C-5262	Sequence 5262, Ap
168	7	1.3	755	4	US-09-642-034-5	Sequence 5, Appli	241	6	1.1	67	3	US-09-134-001C-4786	Sequence 4786, Ap
169	7	1.3	760	4	US-09-252-991A-27790	Sequence 27790, A	242	6	1.1	67	4	US-09-489-039A-10141	Sequence 10141, A
170	7	1.3	778	4	US-09-248-796A-16014	Sequence 16014, A	243	6	1.1	68	4	US-09-252-991A-32975	Sequence 32975, A
171	7	1.3	834	4	US-09-404-967C-5	Sequence 5, Appli	244	6	1.1	69	4	US-09-107-532A-6142	Sequence 6142, Ap
172	7	1.3	877	1	US-08-430-925A-4	Sequence 4, Appli	245	6	1.1	69	4	US-09-248-796A-14723	Sequence 14723, A
173	7	1.3	937	4	US-09-949-016-9286	Sequence 8286, Ap	246	6	1.1	70	4	US-09-621-976-6964	Sequence 6964, Ap

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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:29:52 ; Search time 116.974 Seconds

(without alignments)
1772.222 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 536

Sequence: 1 MAAGAMTPRPVQPARPGF.....LFAKGEVQWALNDHHGRH 536

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : A Genesecp16Dec04:*

- 1: Genesecp1980s:*
- 2: Genesecp1990s:*
- 3: Genesecp2000s:*
- 4: Genesecp2001s:*
- 5: Genesecp2002s:*
- 6: Genesecp2003as:*
- 7: Genesecp2003bs:*
- 8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			Description
	Score	Match	Length DB ID	
1	536	100.0	536	3 AAY45089 Human GBS
2	536	100.0	536	4 AAE06518 Human gro
3	495	92.4	495	3 AAY45087 Partial h
4	495	92.4	495	4 AAB66967 Human AST
5	495	92.4	495	8 ADJ75516 Marker ge
6	495	92.4	495	8 ADRI4587 Human NF-
7	495	92.4	495	8 ADP25217 PRO polyP
8	394	73.5	495	4 AAM38959 Human pol
9	314	58.6	314	4 AAG65238 Human sod
10	304	56.7	309	4 AAM40745 Human pol
11	284	53.0	284	5 ABP41345 Human ova
12	273	50.9	277	8 AAM93914 Human pol
13	273	50.9	277	8 ADJ32036 Human pro
14	217	40.5	272	5 ABB89975 Human pol
15	180	33.6	194	4 AAM25685 Human pro
16	144	26.9	343	4 ABG12999 Novel hum
17	144	26.9	343	6 ABO00820 Polypepti
18	134	25.0	256	4 ABG02032 Novel hum
19	124	23.1	124	4 AAG81307 Human AFP
20	61	11.4	495	3 AAY45088 Sheep GBS
21	61	11.4	495	4 AAE06519 Sheep gro
22	15	2.8	15	4 AAG65239 Human sod
23	14	2.6	495	3 AAY45090 Human/She
24	11	2.1	467	8 ADPI2952 Protein e
25	11	2.1	578	7 ADG88331 Rat trans

99	7	1.3	67	3	AA540211	Aab40211	Gene 17 h	172	7	1.3	163	8	ADM09216	Human TPO
100	7	1.3	76	4	AAU65452	Aau65452	Propionib	173	7	1.3	164	2	AAAR81348	AAAR81348 [Hi633, T
101	7	1.3	76	6	ABM61971	Abm61971	Propionib	174	7	1.3	164	2	AAAR81349	AAAR81349 [Hi633, A
102	7	1.3	78	4	AAU40931	Aau40931	Propionib	175	7	1.3	164	2	AAAR81350	AAAR81350 [Gly116,
103	7	1.3	78	6	ABM37450	Abm37450	Propionib	176	7	1.3	164	2	AAAR81350	AAAR81350 [Hi633, G
104	7	1.3	79	4	AAW95790	Aam95790	Human rep	177	7	1.3	164	2	AAAR81353	AAAR81353 [Gly116,
105	7	1.3	79	4	AB896321	Abb96321	Human tes	178	7	1.3	164	2	AAAR81351	AAAR81351 [Gly116,
106	7	1.3	81	5	ABP08020	Abp08020	Human ORF	179	7	1.3	165	2	AAW04868	AAW04868 Human thr
107	7	1.3	82	4	AAW16057	Aam16057	Peptide #	180	7	1.3	165	2	AAW04868	AAW04868 Human thr
108	7	1.3	82	4	ABB35049	Abb35049	Peptide #	181	7	1.3	165	2	AAW55013	AAW55013 Human will
109	7	1.3	82	4	AAW28554	Aam28554	Peptide #	182	7	1.3	165	2	AAW55013	AAW55013 Human will
110	7	1.3	82	4	AB829865	Abb29865	Peptide #	183	7	1.3	166	2	AAW55013	AAW55013 Human will
111	7	1.3	82	4	AB820461	Abb20461	Protein #	184	7	1.3	171	2	AAW55013	AAW55013 Human will
112	7	1.3	82	4	AAW68235	Aam68235	Human bon	185	7	1.3	171	2	AAW55013	AAW55013 Human will
113	7	1.3	82	4	AAW55864	Aam55864	Human bra	186	7	1.3	171	2	AAW55013	AAW55013 Human will
114	7	1.3	82	4	ABG49886	Abg49886	Human liv	187	7	1.3	175	2	AAW12953	AAW12953 [N30, T32,
115	7	1.3	82	4	AAW03784	Aam03784	Peptide #	188	7	1.3	175	2	AAW12953	AAW12953 [N30, T32,
116	7	1.3	82	5	ABG37771	Abg37771	Human pep	189	7	1.3	176	2	AAW12953	AAW12953 [N30, T32,
117	7	1.3	86	4	AB65993	Aab65993	Human sec	190	7	1.3	176	2	AAW12953	AAW12953 [N30, T32,
118	7	1.3	99	3	AA622278	Aag22278	Arabidops	191	7	1.3	179	5	ABU50929	ABU50929 Helicobac
119	7	1.3	100	4	ABG327184	Abg327184	Novel hum	192	7	1.3	180	2	AAW12953	AAW12953 [N30, T32,
120	7	1.3	102	4	AA622749	Aag22749	S. epider	193	7	1.3	185	1	AAW12953	AAW12953 [N30, T32,
121	7	1.3	103	4	AAW86466	Aam86466	Human imm	194	7	1.3	185	2	AAW12953	AAW12953 [N30, T32,
122	7	1.3	103	6	ADA54545	Ada54545	Human pro	195	7	1.3	185	7	AAW12953	AAW12953 [N30, T32,
123	7	1.3	106	5	ADH32514	Adh32514	Yeast smo	196	7	1.3	186	1	AAW12953	AAW12953 [N30, T32,
124	7	1.3	107	5	ADK36539	Adk36539	Novel hum	197	7	1.3	187	1	AAW12953	AAW12953 [N30, T32,
125	7	1.3	110	8	ADQ66018	Adq66018	Novel hum	198	7	1.3	187	1	AAW12953	AAW12953 [N30, T32,
126	7	1.3	114	2	AAW54390	Aaw54390	Actinomad	199	7	1.3	187	2	AAW12953	AAW12953 [N30, T32,
127	7	1.3	115	5	ABP31660	Abp31660	Human ORP	200	7	1.3	188	2	AAW12953	AAW12953 [N30, T32,
128	7	1.3	119	3	AA622277	Aag22277	Arabidops	201	7	1.3	188	2	AAW12953	AAW12953 [N30, T32,
129	7	1.3	119	3	AA608053	Aag08053	Arabidops	202	7	1.3	188	2	AAW12953	AAW12953 [N30, T32,
130	7	1.3	122	5	AAU81759	Aau81759	Partial p	203	7	1.3	192	8	ABM80182	ABM80182 Tumour-as
131	7	1.3	122	5	ABP40142	Abp40142	Staphyloc	204	7	1.3	192	8	ABM80182	ABM80182 Tumour-as
132	7	1.3	122	8	AD507186	Ad507186	Staphyloc	205	7	1.3	195	2	AAW12953	AAW12953 [N30, T32,
133	7	1.3	126	6	ABU49557	Abu49557	Protein e	206	7	1.3	195	2	AAW12953	AAW12953 [N30, T32,
134	7	1.3	127	4	ABO67023	Ab067023	Klebsiell	207	7	1.3	200	1	AAW12953	AAW12953 [N30, T32,
135	7	1.3	131	4	AAU20576	Aau20576	Human sec	208	7	1.3	200	4	AAW12953	AAW12953 [N30, T32,
136	7	1.3	132	4	AAW59519	Aab59519	Human sec	209	7	1.3	200	4	AAW12953	AAW12953 [N30, T32,
137	7	1.3	132	7	ADW25718	Adm25718	Hyperther	210	7	1.3	202	4	ABW63463	ABW63463 Human GPC
138	7	1.3	133	4	ABG11406	Abg11406	Novel hum	211	7	1.3	202	4	ABW63463	ABW63463 Human GPC
139	7	1.3	135	4	AAW96101	Aam96101	Human rep	212	7	1.3	203	1	AAW96101	AAW96101 Fish grow
140	7	1.3	136	3	AA602129	Aag02129	Human sec	213	7	1.3	203	2	AAW96101	AAW96101 Fish grow
141	7	1.3	145	2	AAW94926	Aaw94926	Human phe	214	7	1.3	203	2	AAW96101	AAW96101 Fish grow
142	7	1.3	150	2	AAW80822	Aar80822	Human MGD	215	7	1.3	204	1	AAW96101	AAW96101 Fish grow
143	7	1.3	152	6	ADA54165	Ada54165	Human pro	216	7	1.3	204	2	AAW96101	AAW96101 Fish grow
144	7	1.3	155	3	AAW53291	Aab53291	Human col	217	7	1.3	204	2	AAW96101	AAW96101 Fish grow
145	7	1.3	155	3	AAW24501	Aab24501	Human col	218	7	1.3	204	2	AAW96101	AAW96101 Fish grow
146	7	1.3	155	4	AAW74756	Aag74756	Human col	219	7	1.3	204	2	AAW96101	AAW96101 Fish grow
147	7	1.3	157	8	ADR10198	Adr10198	Human pro	220	7	1.3	204	5	ABG31737	ABG31737 Yellow gr
148	7	1.3	158	6	AAW97763	Aar97763	Human thr	221	7	1.3	204	7	ABG31737	ABG31737 Yellow gr
149	7	1.3	158	6	ABU35777	Abu35777	Protein e	222	7	1.3	204	7	ABG31737	ABG31737 Yellow gr
150	7	1.3	162	2	AAW81346	Aar81346	[Delta-Ar	223	7	1.3	204	7	ABG31737	ABG31737 Yellow gr
151	7	1.3	162	2	AAW81345	Aar81345	[Delta-Hi	224	7	1.3	206	3	ABW58830	ABW58830 Breast an
152	7	1.3	162	2	AAW81347	Aar81347	[Delta-Gl	225	7	1.3	207	2	AAW58830	AAW58830 Breast an
153	7	1.3	163	2	AAW80825	Aar80825	Human MGD	226	7	1.3	207	2	AAW58830	AAW58830 Breast an
154	7	1.3	163	2	AAW81342	Aar81342	Thrombopo	227	7	1.3	207	5	ABW89411	ABW89411 Human pol
155	7	1.3	163	2	AAW81354	Aar81354	[Alal, Va	228	7	1.3	208	2	AAW89411	AAW89411 Human pol
156	7	1.3	163	2	AAW81373	Aar81373	[Arg59]TP	229	7	1.3	213	2	AAW89411	AAW89411 Human pol
157	7	1.3	163	2	AAW81360	Aar81360	[Alal, Va	230	7	1.3	216	2	AAW89411	AAW89411 Human pol
158	7	1.3	163	2	AAW81359	Aar81359	[Alal, Va	231	7	1.3	217	8	ADW03128	ADW03128 Human nov
159	7	1.3	163	2	AAW81366	Aar81366	[Alal, Va	232	7	1.3	217	8	ADW03128	ADW03128 Human nov
160	7	1.3	163	2	AAW81371	Aar81371	[Leu146]T	233	7	1.3	218	7	ADW03128	ADW03128 Human nov
161	7	1.3	163	2	AAW81374	Aar81374	[Arg115]T	234	7	1.3	222	6	ABW68944	ABW68944 Photococ
162	7	1.3	163	2	AAW81369	Aar81369	[Arg143]T	235	7	1.3	223	3	ABW68944	ABW68944 Photococ
163	7	1.3	163	2	AAW81363	Aar81363	[Alal, Va	236	7	1.3	223	5	AAO15070	AAO15070 Human pro
164	7	1.3	163	2	AAW81368	Aar81368	[Arg133]T	237	7	1.3	223	5	AAO15070	AAO15070 Human pro
165	7	1.3	163	2	AAW81362	Aar81362	[Alal, Va	238	7	1.3	227	3	ADW03128	ADW03128 Human nov
166	7	1.3	163	2	AAW81367	Aar81367	[Arg129]T	239	7	1.3	227	3	ADW03128	ADW03128 Human nov
167	7	1.3	163	2	AAW81370	Aar81370	[Leu82]TP	240	7	1.3	227	4	AAW03128	AAW03128 Human nov
168	7	1.3	163	2	AAW81365	Aar81365	[Alal, Va	241	7	1.3	228	5	AAO15062	AAO15062 Endogluc
169	7	1.3	163	2	AAW81361	Aar81361	[Alal, Va	242	7	1.3	228	5	AAO15062	AAO15062 Endogluc
170	7	1.3	163	2	AAW97769	Aar97769	Human thr	243	7	1.3	228	8	ADL05112	ADL05112 M. catarr
171	7	1.3	163	5	ABB07002	Abb07002	Human c-m	244	7	1.3	232	2	AAAR81343	AAAR81343 Thrombopo

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2005, 03:19:49 ; Search time 4589.43 Seconds
(without alignments)
4105.478 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 2617

Sequence: 1 MKSPVSLAPSGDEGSDRT.....LFAKGEVQNAISDQHGRN 495

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09776865/runat_08072005_175549_23379/app_query.fasta_1.1358
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09776865@cgn_1_1_6461/runat_08072005_175549_23379 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2329	89.0	3189	3 CR618872	full-leng
2	2236	85.4	3202	3 AK029102	Mus muscu
3	1434	54.8	1051	1 AL550137	AL550137
4	1320.5	50.5	1059	5 BX425026	BX425026
5	1310	50.1	1038	5 BX439809	BX439809
6	1291	49.3	737	7 CR833737	CR833737
7	1267	48.4	721	7 CR833565	CR833565
8	1236	47.2	947	7 CO579484	CO579484
9	1128	43.1	773	1 AJ734267	AJ734267

10	1118	42.7	740	6	CB317739	AGENCOURT
11	1108	42.3	730	6	CB327442	UI-M-PYO-
12	1075.5	41.1	901	6	CD106410	AGENCOURT
13	1055	40.3	708	7	CR763802	DKF2P4690
14	1038	39.7	801	4	BI661062	603304362
15	1001	38.2	813	7	CF618610	AGENCOURT
16	1000	38.2	605	5	BX479639	DKF2P686F
17	996	38.1	770	7	CF289959	AGENCOURT
18	988.5	37.8	791	7	CV110989	AGENCOURT
19	986	37.7	913	5	BX348297	EX348297
20	971.5	37.1	831	3	AK087395	Mus muscu
21	964	36.8	4078	3	AK045409	Mus muscu
22	953	36.4	754	4	BI907284	603063858
23	949	36.3	581	5	BP297030	BP297030
24	948	36.2	570	5	BP274537	BP274537
25	945	36.1	663	7	CV023522	483 Full
26	942.5	36.0	776	5	BX882862	EX882862
27	928.5	35.5	2014	3	AK082743	Mus muscu
28	921	35.2	626	2	BF676817	602084380
29	915	35.0	711	4	BI697765	603346858
30	903	34.5	582	5	BF302998	BP302998
31	903	34.5	630	6	CB138761	K-EST0191
32	903	34.5	770	5	BX674896	EX674896
33	900	34.4	1531	3	BC023331	Mus muscu
34	890	34.0	649	1	AJ734277	AJ734277
35	885	33.8	611	1	AJ734276	AJ734276
36	884.5	33.8	4630	3	AK040717	Mus muscu
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38	877	33.5	700	7	CN786597	4120614 B
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45	859	32.8	618	7	CF170114	B0822G02-

ALIGNMENTS

CR618872 3189 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DI040YK17 of Placenta Cot 25-normalized
of Homo sapiens (human).

ACCESSION CR618872

VERSION CR618872.1 GI:50499679

KEYWORDS HTC; CDS; EST; cDNA

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600

REFERENCE 2 (bases 1 to 3189)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES Location/Qualifiers

source

1..3189

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ORIGIN

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 Best Local Similarity: 86.26% Mismatches: 29
 Query Match: 89.00% Indels: 0
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US-09-776-865-4 (1-495) x CR618872 (1-3189)

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 Db 136 CCTCTTCTACCGGGCGGCCCGCCGAGCGGCTCCAGGTGCTGCTCTGCTCGTTAC 195
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 AK029102
 ACCESSION AK029102.1 GI:26325087
 VERSION
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1
 REFERENCES
 1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 MEDLINE
 11042159
 PUBMED
 3
 REFERENCES
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2005, 07:16:14 ; Search time 840.684 Seconds
(without alignments)
3696.712 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 2617

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Searched: 6330943 seqs, 3139157217 residues

Total number of hits satisfying chosen parameters: 12661886

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA:*

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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; TITLE OF INVENTION: Methods for Preventing or Attenuating Pathoangiogenic Conditions
; FILE REFERENCE: 22100-0100 46126-252687
; CURRENT APPLICATION NUMBER: US/09/776,865
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,870
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2844

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; TYPE: DNA
; ORGANISM: Ovis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)..(1568)
US-09-776-865-3

Alignment Scores:
Pred. No.: 6,74e-271 Length: 2844
Score: 2617.00 Matches: 495
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-776-865-4 (1-495) x US-09-776-865-3 (1-2844)

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RESULT 2
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; APPLICANT: Hellerqvist, Carl
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/01US
; CURRENT APPLICATION NUMBER: US/10/823,506
; PRIOR FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/359,167
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-693,843
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 2844
; TYPE: DNA
; ORGANISM: Ovis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)..(1568)
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)

3464.068 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 2617

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFWT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPTXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPELLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2617	100.0	2844	US-09-359-167-3	Sequence 3, Appli
2	2329	89.0	2513	US-09-949-016-1834	Sequence 1834, Ap
3	2329	89.0	2602	US-09-359-167-1	Sequence 1, Appli
4	2329	89.0	2930	US-09-359-167-7	Sequence 7, Appli
5	2221	84.9	1485	US-09-359-167-9	Sequence 9, Appli
6	1971	75.3	1485	US-09-359-167-11	Sequence 11, Appli
7	980	37.4	1811	US-09-740-041-1	Sequence 1, Appli
8	956.5	36.5	2607	US-09-915-181A-1	Sequence 1, Appli
9	932	35.6	2366	US-09-949-016-5483	Sequence 5483, Ap
10	931	35.6	2716	US-08-647-484-1	Sequence 1, Appli
11	931	35.6	2716	US-08-647-484-3	Sequence 3, Appli
12	931	35.6	2716	US-08-647-481-1	Sequence 1, Appli

13	931	35.6	2716	1	US-08-647-481-3	Sequence 3, Appli
14	931	35.6	2716	1	US-08-430-033A-1	Sequence 1, Appli
15	931	35.6	2716	1	US-08-430-033A-3	Sequence 3, Appli
16	931	35.6	2716	5	PCT-US96-05792-1	Sequence 1, Appli
17	931	35.6	2716	5	PCT-US96-05792-3	Sequence 3, Appli
18	874.5	33.4	2626	4	US-09-949-016-745	Sequence 745, App
19	761	29.1	2612	4	US-09-270-767-13970	Sequence 13970, A
20	753	28.8	2265	2	US-08-724-394A-18	Sequence 18, Appl
21	753	28.8	2270	4	US-09-949-016-5577	Sequence 5577, Ap
22	738	28.2	1229	4	US-09-023-655-660	Sequence 660, App
23	621.5	23.7	2296	4	US-09-949-016-1182	Sequence 1182, Ap
24	605.5	23.1	1643	2	US-08-805-118-2	Sequence 2, Appli
25	605.5	23.1	1643	3	US-09-391-958-2	Sequence 2, Appli
26	605.5	23.1	1780	2	US-08-724-394A-19	Sequence 19, Appl
27	450	17.2	1383	4	US-08-489-039A-2492	Sequence 2492, Ap
28	442	16.9	1699	4	US-09-799-451-815	Sequence 815, App
29	428.5	16.4	1074	4	US-09-270-767-13957	Sequence 13957, A
30	398	15.2	3486	4	US-09-976-594-1018	Sequence 1018, Ap
31	389	14.9	976	4	US-09-270-767-13814	Sequence 13814, A
32	385.5	14.7	1413	4	US-09-328-352-2786	Sequence 2786, Ap
33	385.5	14.0	1368	4	US-08-489-039A-2771	Sequence 2771, Ap
34	365	13.9	1317	3	US-09-172-952-5	Sequence 5, Appli
35	365	13.9	1500	4	US-09-922-501-11	Sequence 11, Appl
36	365	13.9	9334	3	US-09-172-952-19	Sequence 19, Appl
37	363	13.9	63783	4	US-09-949-016-13576	Sequence 13576, A
38	360	13.8	471	4	US-09-270-767-30032	Sequence 30032, A
39	357	13.6	217	4	US-09-016-434-602	Sequence 602, App
40	353	13.5	1305	4	US-09-489-039A-6462	Sequence 6462, Ap
41	341	13.0	492	4	US-09-270-767-1297	Sequence 1297, Ap
42	341	13.0	492	4	US-09-270-767-16579	Sequence 16579, A
43	338.5	12.9	1269	4	US-09-891-641-65	Sequence 65, Appl
44	326.5	12.5	1380	4	US-09-489-039A-3459	Sequence 3459, Ap
45	318	12.2	1600	4	US-09-922-501-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-359-167-3
; Sequence 3, Application US/09359167
; Patent No. 6803448
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/0105
; CURRENT APPLICATION NUMBER: US/09/359,167
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 60-693,843
; EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2844
; TYPE: DNA
; ORGANISM: Ovis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)..(1568)
US-09-359-167-3

Alignment Scores:
Pred. No.: 9,11e-302 Length: 2844
Score: 2617.00 Matches: 495
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-776-865-4 (1-495) x US-09-359-167-3 (1-2844)

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Qy 21 ProLeuLeuGlnArgAlaProArgAlaGluProAlaProValCysCysSerAlaArgTyr 40
Db 144 CGCTCTCGACGGCGCGCGCGGCGGACCCGCTCCAGTATGCTGCTCTGCTGTAC 203
Qy 41 AenLeuAlaPheLeuSerPhePheGlyPhePheValLeuTyrSerLeuArgValAsnLeu 60
Db 204 AACCTAGCATTCTTCT 263
Qy 61 SerValAlaLeuValAspMetValAspSerAsnThrThrAlaLysAspAsnArgThrSer 80
Db 264 AGCGTGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 323
Qy 81 TyrGluCysAlaGluHisSerAlaProIleLysValLeuHisAsnGlnThrGlyLysLys 100
Db 324 TAGGAGTGTGACAGCATCTGCTCCCATAAAGTCTTCCACCAACCGGTTAAAG 383
Qy 101 TyrArgTyrAspAlaGluThrGlnGlyTyrIleLeuGlySerPhePheTyrGlyTyrIle 120
Db 384 TACCGGTGGGATGCAGAACTCAAGATGATCTCGGATCTTTCTCTATGGCTACATC 443
Qy 121 IleThrGlnIleProGlyGlyTyrValAlaSerArgSerGlyGlyLysLeuLeuGly 140
Db 444 ATCACACAAATTCCTGGAGGATATGTTGCCAGCAAGTGGGGGAAGCTGTGCTAGGA 503
Qy 141 PheGlyIlePheAlaThrAlaIlePheThrLeuPheThrProLeuAlaAlaAspPheGly 160
Db 504 TTCGGGATCTTGTACAGCTATCTTCCACCTGTTCACCTCCCTCGCTGCAGATTTCGA 563
Qy 161 ValGlyAlaLeuValAlaLeuArgAlaLeuGluGlyLeuGlyGluGlyValThrTyrPro 180
Db 564 GTCCGAGCCCTGTTGCACTCAGGCACTAGAAAGGCTAGGAGGGGTGCACATATCCA 623
Qy 181 AlaMetHisAlaMetTyrSerSerTyrAlaProProLeuGluArgSerLysLeuLeuSer 200
Db 624 GCCATGATGCATGCTGCTTTCATGGGCTCCCCCTCTTGAAGAAGCAAGCTTCTGAGT 683
Qy 201 IleSerTyrAlaGlyAlaGlnLeuGlyThrValValSerLeuProLeuSerGlyValIle 220
Db 684 ATTTCAATATGCGAGGACCACTTGGGACAGTAGTTCTCTCTCTCTCTCTCTCTCTCT 743
Qy 221 CysTyrTyrMetAsnTyrThrTyrValPheTyrPhePheGlyIleValGlyIleIleTyr 240
Db 744 TGCTACTATGAATGGACATATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 803
Qy 241 PheIleLeuTyrIleCysLeuValSerAspThrProGluThrHisLysThrIleThrPro 260
Db 804 TTTATTTTATGGATCTGCTTATGTTAGTGATACCCAGAACTCACAAGACCAATCACTCC 863
Qy 261 TyrGluLysGluTyrIleLeuSerSerLeuLysAsnGlnLeuSerSerGlnLysSerVal 280
Db 864 TATGAAAGGAGTATATTTCTTTCATCATTAATAATCAGCTCTCTTTCACAGAGTCAGT 923
Qy 281 ProTyrIleProMetLeuLysSerLeuProLeuTyrAlaIleValValAlaHisPheSer 300
Db 924 CGTGGATACCTATGCTGAAATCACTGCCACTTTGGGCTATTGCTGTTGCACATTTTCT 983
Qy 301 TyrAsnTyrThrPheTyrThrLeuLeuThrLeuLeuProThrTyrMetLysGluValLeu 320
Db 984 TACAACTGGACTTTTATACCTTTGTGACCTTATTTGCCCTATTTACATGAAGGAATCCTA 1043
Qy 321 ArgPheAsnIleGlnGluAsnGlyPheLeuSerAlaValProTyrLeuGlyCysTyrLeu 340
Db 1044 AGTTCAATATTCAGAGATGGGTTTTTATCTGAGTCCCTTATTTAGTTTGTGTTA 1103
Qy 341 CysMetIleLeuSerGlyGlnAlaAlaAspAsnLeuArgAlaArgTyrAsnPheSerThr 360
Db 1104 TGTATGATCTGTCCGGTCAAGCTGCTGACAAATTTAAGGGCAAGATGAAATTTTCAACT 1163
Qy 361 LeuTyrValArgArgValPheSerLeuIleGlyMetIleGlyProAlaIlePheLeuVal 380
Db 1164 CTGTGGGTTCGAAGAGTTTTTAGCCTTATAGGATGATTTGGACCTGCGATATTTCTGTT 1223

Qy 381 AlaAlaGlyPheIleGlyCysAspTyrSerLeuAlaValAlaPheLeuThrIleSerThr 400
Db 1224 GCCGACGAGTTTATAGCTGTGATTATTTCTTTGGCTGTTCATCTCTTAACCATATCAACA 1283
Qy 401 ThrLeuGlyGlyPheCysSerSerGlyPheSerIleAsnHisLeuAspIleAlaProSer 420
Db 1284 ACCCTGGAGGCTTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1343
Qy 421 TyrAlaGlyIleLeuLeuGlyIleThrAsnThrPheAlaThrIleProGlyMetIleGly 440
Db 1344 TATCTGGTATTTCTCTGGGATCACAATACCTTTGCCACTATTTCTGGAAATGATTGGG 1403
Qy 441 ProIleAlaAlaArgSerLeuThrProGluAsnThrIleGlyGluTyrGlnThrValPhe 460
Db 1404 CCATCATTTGCCAGAGTCTTACCCCTGAGACACATATTGAGAAATGGCAACTGTTTTC 1463
Qy 461 CysIleAlaAlaAlaIleAsnValPheGlyAlaIlePhePheThrLeuPheAlaLysGly 480
Db 1464 TGCATCGCTGCTGCTATCAATGATTTTGGTGCCATTTTCTTCACTATTTCGCCAAAGT 1523
Qy 481 GluValGlnAsnTyrAlaIleSerAspHisGlnGlyHisArgAsn 495
Db 1524 GAAGTGCAAAACTGGGCTATCAGTGATCACCAGGACACAGAAAC 1568

RESULT 2

US-09-949-016-1834
; Sequence 1834, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1834
; LENGTH: 2513
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1834

Alignment Scores:

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Percent Similarity:	94.14%	Conservative:	39
Best Local Similarity:	86.26%	Mismatches:	29
Query Match:	89.00%	Indels:	0
DB:	4	Gaps:	0

US-09-776-865-4 (1-495) x US-09-949-016-1834 (1-2513)

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Db 272 ATGAGGCTCCGGTTCGAGACCTGGCCCGGAACGATGGCGAGGAGAGCAGCGACGACG 331
Qy 21 ProLeuLeuGlnArgAlaProArgAlaGluProAlaProValCysCysSerAlaArgTyr 40
Db 332 CCTCTTCTACGGGCGCCCAACCGGCGCAAGCCCTCCAGTGTCTCTCTGCTCGTTAC 391
Qy 41 AsnLeuAlaPheLeuSerPhePhePheValLeuTyrSerLeuArgValAsnLeu 60
Db 392 AACTTACCAATTTGGCTTTTGGTTTCTTCACTGTGTATGATGATGATGATGATGATG 451
Qy 61 SerValAlaLeuValAspMetValAspSerAsnThrThrAlaLysAspAsnArgThrSer 80

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: July 9, 2005, 02:43:23 ; Search time 742.26 Seconds
(without alignments)
3947.771 Million cell updates/sec

Title: US-09-776-865-4
Perfect score: 2617
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseq2003bs.*
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11: geneseq2003ds.*
12: geneseq2004as.*
13: geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2617	100.0	2844	3 AAZ50876	Aaz50876 Sheep GBS
2	2617	100.0	2844	4 AAD10326	Aad10326 Sheep gro
3	2329	89.0	2511	12 ADQ84158	Adq84158 Human tum
4	2329	89.0	2512	4 AAF55900	Aaf55900 Human AST
5	2329	89.0	2602	3 AAZ50875	Aaz50875 Partial h

6	2329	89.0	2626	11 ACN91332	ACn91332 Breast ca
7	2329	89.0	2930	3 AAZ50879	Aaz50879 Full leng
8	2329	89.0	2930	4 AAD10325	Aad10325 Human gro
9	2329	89.0	3329	12 ADQ75057	Adq75057 Marker ge
10	2329	89.0	3329	13 ADRI4586	Adri4586 Human NF-
11	2329	89.0	3329	13 ADP25216	Adp25216 PRO polyp
12	2329	89.0	3362	5 ADL45207	Adl45207 Human ova
13	2322	88.7	1488	4 AAI58115	Aai58115 Human pol
14	2302	88.0	2712	4 AAK94876	Aak94876 Human ful
15	2302	88.0	2712	12 ADL32035	Adl32035 Full leng
16	2221	84.9	1485	3 AAZ50880	Aaz50880 Human/She
17	1971	75.3	1485	3 AAZ50881	Aaz50881 Human/She
18	1578	60.3	2670	4 AAH79234	Aah79234 Human sod
19	1386	53.0	1872	6 ABQ54422	Abq54422 Human ova
20	1380	52.7	1651	6 ABL90384	AbL90384 Human pol
21	1217	46.5	929	4 AAI59901	Aai59901 Human pol
22	1104	42.2	853	4 AAK93901	Aak93901 Human CDN
23	1104	42.2	853	12 ADL30328	Adl30328 3' end of
24	1022.5	39.1	838	4 AAK92364	Aak92364 Human CDN
25	1022.5	39.1	838	12 ADL28791	Adl28791 5' end of
26	981.5	37.9	1939	4 ABL03769	AbL03769 Drosophil
27	985.5	37.7	1641	4 ABL18113	AbL18113 Drosophil
28	985.5	37.7	1786	4 ABL07417	AbL07417 Drosophil
29	981.5	37.5	4899	4 ABL03768	AbL03768 Drosophil
30	980	37.4	1811	6 ABK87049	Abk87049 Human tra
31	980	37.4	1811	10 ADG88328	Adg88328 Human tra
32	979	37.4	1767	10 ADD01393	Add01393 Human TCH
33	979	37.4	1850	10 ADD01409	Add01409 Human TCH
34	979	37.4	3671	9 AAL62505	Aal62505 Human tra
35	979	37.4	3952	13 ADR08065	Adr08065 Full leng
36	969.5	37.0	1803	10 ADD01411	Add01411 Mouse TCH
37	969.5	37.0	1822	10 ADD01422	Add01422 Mouse TCH
38	969	37.0	2528	8 ABX13555	Abx13555 Murine DN
39	969	37.0	2528	10 ADC15493	Adc15493 Mouse DNP
40	968	37.0	3982	8 ABX13554	Abx13554 Rat DNP1
41	968	37.0	3982	9 ACF25330	Acf25330 Rat Na-de
42	968	37.0	3982	10 ADC15491	Adc15491 Rat DNPI
43	963.5	36.8	3946	8 ABX13553	Abx13553 Human DNP
44	963.5	36.8	3946	10 ADC15489	Adc15489 Human DNP
45	958	36.6	1701	10 ADJ95071	Adj95071 Novel NOV

ALIGNMENTS

RESULT 1
AAZ50876
ID AAZ50876 standard; cDNA; 2844 BP.
XX
AC AAZ50876;
XX
DT 31-MAY-2000 (first entry)
XX
DE Sheep GBS toxin receptor (SP55) cDNA.
KW Sheep GBS toxin receptor; group B beta-haemolytic streptococci; SP55;
KW pathological vascularisation; cancer metastases; angiogenesis;
KW neovascularisation; reperfusion injury; scarring; keloid;
KW chronic inflammation; rheumatoid arthritis; psoriasis; neural injury;
KW endothelial cell proliferation; antibacterial; anticancer;
KW anti-angiogenic; anti-inflammatory; anti-arthritis; anti-psoriatic; ss.
XX Ovis sp.
XX
FH Key Location/Qualifiers
CDS 84..1571
FT /*tag= a
FT /product= "Sheep GBS toxin receptor"
XX

WO200005375-A1.

03-FEB-2000.

22-JUL-1999; 99WO-US016676.

XX PR 22-JUL-1998; 98US-0093843P.
XX PA (UYVA-) UNIV VANDERBILT.
XX PI Hellerqvist CG, Fu C;
XX WPI; 2000-205377/18.
DR P-PSDB; AAY45088.
XX New polynucleotide encoding mammalian receptor for streptococcus toxin,
PT useful for diagnosis and treatment of, e.g. pneumonia in neonates.
XX
PS Claim 3; Page 83-86; 109pp; English.
CC The present cDNA sequence encodes partial sheep GBS (group B beta -
CC haemolytic streptococci) toxin receptor (SP55). This sequence was cloned
CC using a primary culture of sheep lung endothelial cells. Expression
CC vectors comprising this cDNA can be transformed into host cells to
CC express GBS toxin receptor and its fragments. Detecting the receptor in
CC tissues is used to diagnose pathological vascularisation, e.g. for
CC detecting cancer metastases. GBS toxin receptors are useful for treating
CC conditions associated with pathological angiogenesis or
CC neovascularisation (specifically cancer, reperfusion injury, scarring
CC during wound healing, keloids, chronic inflammation (rheumatoid arthritis
CC or psoriasis) or neural injury), and to raise specific antibodies used
CC for treating early onset disease. Inhibitors of this receptor are useful
CC for treating pathological or hypoxia-induced endothelial cell
CC proliferation and migration
XX
SQ Sequence 2844 BP; 745 A; 623 C; 594 G; 882 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,99e-256 Length: 2844
Score: 2617.00 Matches: 495
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-776-865-4 (1-495) x AAZ50876 (1-2844)

QY 1 MetIysSerProValSerAspLeuAlaProSerAspGlyGluGlySerAspArgThr 20
Db 84 ATGAAGTCCCGGTTTCGGACTTAGCCCCGAGCGACGCGAGGAGGCGCGACCA 143

QY 21 ProLeuLeuGlnArgAlaProArgAlaGluProAlaProValCysCysSerAlaArgThr 40
Db 144 CCGCTCCCTGCAGCGCGCGCGCGCGCGGAAACCGCTCCAGTATGCTGCTCGTTAC 203

QY 41 AsnLeuAlaPheLeuSerPheGlyPhePheValLeuTyrSerLeuArgValAsnLeu 60
Db 204 AACCTAGCATTTTGTCTTTTGGTTTCTGCTTCTCTATTCATTACGGGTGAACTG 263

QY 61 SerValAlaLeuValAspMetValAspSerAsnThrThrAlaLysAspAsnArgThrSer 80
Db 264 AGCGTTGCACCTAGTGGACATGGTGGATTCAAAACCAACTGCGCAAGATAATAGAAGTCC 323

QY 81 TyrGluCysAlaGluHisSerAlaProIleLysValLeuHisAsnGlnThrGlyLysLys 100
Db 324 TACGAGTGTGCAGAGCATCTGCTCCCAATAAAGTTCTCAACCAACCGGGTAAAG 383

QY 101 TyrArgTrpAspAlaGluThrGlnGlyTrpIleLeuGlySerPhePheTyrGlyTyrIle 120
Db 384 TACCGTGGGATGCAGAACTCAAGATGGATTCTCGGATCTTTTCTATGGCTACATC 443

QY 121 IleThrGlnIleProGlyGlyTyrValAlaSerArgSerGlyGlyLysLeuLeuGly 140
Db 444 ATCACAAAATTCCTGGAGGATATGTTGCCAGCAGAGTGGGGGAGAGCTGTTGCTAGGA 503

QY 141 PheGlyIlePheAlaThrAlaIlePheThrLeuPheThrProLeuAlaAlaAspPheGly 160
Db 504 TTCGGGATCTTTGTACAGCTATCTTACCCCTGTTCACCTCCCTCGCTGCAGATTTCCGA 563

QY 161 ValGlyAlaLeuValAlaLeuArgAlaLeuGluGlyLeuGlyGluGlyValThrTyrPro 180
Db 564 GTCGGAGCCCTTGTTCACCTCAGGGCCTAGAGGGCTAGGAGGGGTGTCCACATATCCA 623

QY 181 AlaMetHisAlaMetTrpSerSerTrpAlaProProLeuGluArgSerLysLeuLeuSer 200
Db 624 GCCATGCATGCCATGTGTCTTCATGGGCTCCCTCTTGAAGAAGCAAGCTTCTGAGT 683

QY 201 IleSerTyrAlaGlyAlaGlnLeuGlyThrValValSerLeuProLeuSerGlyValIle 220
Db 684 ATTTTCATATGAGGAGCACAACTTGGGACAGTAGTTCTCTCTCTTCTTCTGGAGTAAT 743

QY 221 CysTyrTyrMetAsnTrpThrTyrValPheTyrPhePheGlyIleValGlyIleIleTrp 240
Db 744 TGCTACTATATGAATGGACTTATGTCTCTTATTTCTTGGCATTTTGGAAATCATCTGG 803

QY 241 PheIleLeuTrpIleCysLeuValSerAspThrProGluThrHisLysThrIleThrPro 260
Db 804 TTTATTTTATGGATCTGCTTAGTTAGTATACACAGAACTCAAGAACAATCACTCCC 863

QY 261 TyrGluLysGluTyrIleLeuSerSerLeuLysAsnGlnLeuSerSerGlnLysSerVal 280
Db 864 TATGAAAGGAGTATATTTCTTCATCAATAAAAAATCAGCTCTCTTCCACAGAACTCAGT 923

QY 281 ProTrpIleProMetLeuLysSerLeuProLeuTrpAlaIleValAlaHisPheSer 300
Db 924 CCGTGGATACCTATGCTGAAATCACTGCCACTTTGGGCTATTGTGCTGCACATTTTCT 983

QY 301 TyrAsnTrpThrPheTyrThrLeuLeuThrLeuLeuProThrTyrMetLysGluValLeu 320
Db 984 TACAACCTGGACTTTTATATCTTTGTGACCTTATTGCTACTTACATGAAGGAAGTCCTA 1043

QY 321 ArgPheAsnIleGlnGluAsnGlyPheLeuSerAlaValProTyrLeuGlyCysTrpLeu 340
Db 1044 AGGTTCAATATTCAAGAGATGGGTTTTTATCTGACGCTCCCTTATTAGGTGTGTGTTA 1103

QY 341 CysMetIleLeuSerGlyGlnAlaAlaAspAsnLeuArgAlaArgTrpAsnPheSerThr 360
Db 1104 TGTATGATCCTGCGGCTCAAGCTGCTGACATTTTAAGGGCAAGATGGAATTTTCACT 1163

QY 361 LeuTrpValArgArgValPheSerLeuIleGlyMetIleGlyProAlaIlePheLeuVal 380
Db 1164 CTGTGGGTTCCGAGAGATTTTATAGCTTTATAGGGATGATTGGACCTGGATATTCCTGTT 1223

QY 381 AlaAlaGlyPheIleGlyCysAspTyrSerLeuAlaValAlaPheLeuThrIleSerThr 400
Db 1224 GCGCAGATTTATAGGCTGTGATTATCTCTTGGCTGTGATTTCTTAACCATATCAACA 1283

QY 401 ThrLeuGlyGlyPheCysSerSerGlyPheSerIleAsnHisLeuAspIleAlaProSer 420
Db 1284 ACCCTGGAGGCTTTTGTCTCTCTGGATTTAGCATCAACCATCTGGACATTCCTCTCG 1343

QY 421 TyrAlaGlyIleLeuLeuGlyIleThrAsnThrPheAlaThrIleProGlyMetIleGly 440
Db 1344 TATGCTGGTATCTCTCTGGGCATCACAAATACCTTTGCCACTATTCCTGGAATGATTTGG 1403

QY 441 ProfileAlaArgSerLeuThrProGluAsnThrIleGlyGluTrpGlnThrValPhe 460
Db 1404 CCCATCAATGCCAGAGCTTTACCCCTGAGAACACATATTGGAGAAATGGCAAACTGTTTC 1463

QY 461 CysIleAlaAlaAlaIleAsnValPheGlyValaIlePhePheThrLeuPheAlaLysGly 480
Db 1464 TGCATCGCTGCTATCAATGATTATTGGTGCCATTTTCTTCACACTATTTCGCCAAAGGT 1523

QY 481 GluValGlnAsnTrpAlaIleSerAspHisGlnGlyHisArgAsn 495
Db 1524 GAAGTGCAAACTGGGCGCATCAGTGATCAACCAAGGACACAGAAAC 1568

RESULT 2
AAD10326
ID AAD10326 standard; DNA; 2844 BP.
XX

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2005, 02:51:19 ; Search time 6301.05 Seconds
(without alignments)
3806.563 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 2617

Sequence: 1 MKPSVSDLPASDGERGSDRT.....LPAKGEVQWAIHQHGRN 495

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09776865/runat_08072005_175549_23371/app_query.fasta_1.1358
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09776865 @CGN_1_1_8225 @runat_08072005_175549_23371 -NCPUP=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2617	100.0	2844	4	AF244578	AF244578 Ovis arie
2	2617	100.0	2844	6	BD248126	BD248126 GBS toxin
3	2617	100.0	2844	6	AX207626	AX207626 Sequence
4	2329	89.0	2512	6	AX138494	AX138494 Sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	2329	89.0	2512	9	HSA387747	AD387747 Homo sapi
6	2329	89.0	2602	6	BD248125	BD248125 GBS toxin
7	2329	89.0	2930	6	BD248129	BD248129 GBS toxin
8	2329	89.0	2930	6	AX207624	AX207624 Sequence
9	2329	89.0	2930	9	AF244577	AF244577 Homo sapi
10	2329	89.0	3292	9	BC020961	BC020961 Homo sapi
11	2329	89.0	3329	6	CQ776623	CQ776623 Sequence
12	2329	89.0	3362	6	CQ412026	CQ412026 Sequence
13	2302	88.0	2712	6	CQ783928	CQ783928 Sequence
14	2302	88.0	2712	6	BD127905	BD127905 Primer fo
15	2302	88.0	2712	9	AK075320	AK075320 Homo sapi
16	2068	79.0	1485	6	BD248130	BD248130 GBS toxin
17	2068	79.0	3152	10	BC058785	BC058785 Mus muscu
18	2022	77.3	3121	5	AJ719840	AJ719840 Gallus ga
19	1971	75.3	1485	6	BD248131	BD248131 GBS toxin
20	1121	42.8	1963	3	AK114957	AK114957 Ciona int
21	1104	42.2	853	6	CQ782221	CQ782221 Sequence
22	1104	42.2	853	6	BD126930	BD126930 Primer fo
23	1081.5	41.3	2019	3	AK114801	AK114801 Ciona int
24	1022.5	39.1	838	6	CQ780684	CQ780684 Sequence
25	1022.5	39.1	838	6	BD125393	BD125393 Primer fo
26	991.5	37.9	1939	6	CQ575136	CQ575136 Sequence
27	985.5	37.7	1641	6	CQ596652	CQ596652 Sequence
28	985.5	37.7	1786	6	CQ580608	CQ580608 Sequence
29	985.5	37.7	1841	3	AY060776	AY060776 Drosophil
30	981.5	37.5	4899	6	CQ575135	CQ575135 Sequence
31	981.5	37.5	3344	2	AC014246	AC014246 Drosophil
32	981.5	37.5	167926	3	AC023685	AC023685 Drosophil
33	981.5	37.5	174157	3	AC023711	AC023711 Drosophil
34	981.5	37.5	332029	3	AE003491	AE003491 Drosophil
35	981	37.5	2085	3	BT010092	BT010092 Drosophil
36	980	37.4	1811	6	AR316881	AR316881 Sequence
37	980	37.4	1811	6	AX711883	AX711883 Sequence
38	979	37.4	3838	9	HSA459241	AJ459241 Homo sapi
39	979	37.4	3952	6	CQ851102	CQ851102 Sequence
40	979	37.4	3952	9	AK128319	AK128319 Homo sapi
41	976	37.3	1767	10	AV117026	AV117026 Rattus no
42	976	37.3	3172	10	RN0491795	AY491795 Rattus no
43	969.5	37.0	1856	10	AF510321	AF510321 Mus muscu
44	969.5	37.0	4481	10	BC042593	BC042593 Mus muscu
45	969	37.0	2528	6	AX709538	AX709538 Sequence

ALIGNMENTS

RESULT 1	AF244578	Ovis aries	membrane glycoprotein SP55 (sp55) mRNA, complete cds.	2844 bp	mRNA	linear	MAM 06-AUG-2000
LOCUS	AF244578	Ovis aries	membrane glycoprotein SP55 (sp55) mRNA, complete cds.				
DEFINITION	AF244578	Ovis aries	membrane glycoprotein SP55 (sp55) mRNA, complete cds.				
ACCESSION	AF244578	Ovis aries	membrane glycoprotein SP55 (sp55) mRNA, complete cds.				
VERSION	AF244578.1	GI:9719375					
KEYWORDS							
SOURCE		Ovis aries (sheep)					
ORGANISM		Ovis aries					
REFERENCE	1	(bases 1 to 2844)					
AUTHORS		Fu, C., Bardhan, S., Cetateanu, N.D., Lloyd, S.R., Yan, H., P., Carter, C.E., Shi, E., Venkov, C., Yakes, M.F., Page, D.L. and H.C.G.					
TITLE		Identification of a novel membrane protein from mammalian cells that interact with the anti-pathogenic compound CM101					
JOURNAL		Unpublished					
REFERENCE	2	(bases 1 to 2844)					
AUTHORS		Fu, C., Bardhan, S., Cetateanu, N.D., Lloyd, S.R. and Heltqvist, C.G.					
TITLE		Direct Submission					
JOURNAL		Submitted (13-MAR-2000) Biochemistry, Vanderbilt University, School of Medicine, 23rd@Pierce, Nashville, TN 37232-0146, USA					
FEATURES		Location/Qualifiers					
source		1. .2844					
		/organism="Ovis aries"					
		/mol_type="mRNA"					
		/db_xref="taxon:9940"					

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2005, 03:19:49 ; Search time 4969.57 Seconds
(without alignments)
4105.478 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 2836

Sequence: 1 MAAGAMTTPRPQPARPGGF.....LFAKGEVQNWALNDHGHHRH 536

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09776865/runat_08072005_175549_23379/app_query.fasta_1.1358
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09776865@cgn_1.1.6461@runat_08072005_175549_23379 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOB=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2752	97.0	3189	CR618872	CR618872 full-length
2	2312	81.5	3202	AK029102	AK029102 Mus muscu
3	1772	62.5	1051	AL550137	AL550137 AL550137
4	1699.5	59.9	1059	BL425026	BL425026 BX425026
5	1651	58.2	1038	BM439809	BM439809 BX439809
6	1347	47.5	947	CO579484	CO579484 ILLUMIGEN
7	1236	43.6	754	BI907284	BI907284 603063858
8	1193	41.7	737	CK833737	CK833737 4057771 B
9	1174.5	41.4	901	CD106410	CD106410 AGENCOURT

10	1170	41.3	721	7	CK833565
11	1166	41.1	708	7	CR763802
12	1137	40.1	773	1	AJ734267
13	1129	39.8	730	6	CA327442
14	1120	39.5	740	6	CB317739
15	1115	39.3	801	4	BI661062
16	1101.5	38.8	663	7	CV023522
17	1075	37.9	813	7	CF618610
18	1062	37.4	676	2	BE867611
19	1057.5	37.3	791	7	CV110989
20	1056	37.2	913	5	BX348297
21	1051.5	37.1	831	3	AK087395
22	1051	37.1	605	5	BX479639
23	1041.5	36.7	736	5	BP223105
24	1024.5	36.1	736	4	BI860521
25	1015.5	35.8	770	7	CF289359
26	1015	35.8	582	5	BP302998
27	1014	35.8	584	5	BP288606
28	1010	35.6	581	5	BP298092
29	1008	35.5	1007	4	BM804862
30	1003	35.4	582	5	BP287958
31	1002	35.3	583	4	BM838178
32	1001	35.3	581	5	BP297030
33	995	35.1	579	5	BP344739
34	995	35.1	602	5	BP349262
35	994	35.0	581	5	BP281761
36	991	34.9	570	5	BP274537
37	991	34.9	626	2	BF676817
38	991	34.9	711	4	BI697765
39	990	34.9	580	5	BP285113
40	985	34.7	582	5	BP287215
41	979	34.5	582	5	BP367879
42	978	34.5	616	5	BP238694
43	975	34.4	581	5	BP285186
44	975	34.4	582	5	BP288187
45	973	34.3	630	6	CB138761

ALIGNMENTS

CR618872 3189 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DI040YK17 of Placenta Cot 25-normalized
of Homo sapiens (human).

CR618872

CR618872.1 GI:50499679

HTC; CNSLT cDNA.

Source Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue

REFERENCE 2 (bases 1 to 3189)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES Location/Qualifiers

source 1..3189 /organism="Homo sapiens"

/mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1040YK17"
 /tissue_type="Placenta Cot 25-normalized"
 /plasmid="pCWSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 1.22e-270 Length: 3189
 Score: 2752.00 Matches: 520
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 97.04% Indels: 0
 DB: 3 Gaps: 0

US-09-776-865-2 (1-536) x CR618872 (1-3189)

QY 17 ProGlyGlyPheGlyLeuSerGlyArgArgSerLeuLeuGlyGlnValAlaSerThrPro 36
 Db 1 CCGGGGGCTCGGGCTGTGGGGCGGGCTCCCTTCTGCGAGGTGGCGAGTACACCT 60
 QY 37 AlaHisValGlyValMetArgSerProValArgAspLeuAlaAtgAsnAspGlyGluGlu 56
 Db 61 GCTCAGTAGGGCTCATGAGGCTCCGGTTCGAGACCTGGCCCGAAGCATGGCGAGGAG 120
 QY 57 SerThrAspArgThrProLeuLeuProGlyAlaProArgAlaGluAlaAalaProValCys 76
 Db 121 AGCAGCGGCGCACGCTCTTCTACGGGGCGGCCCAACGGCGGCGCTCCAGTGTGC 180
 QY 77 CysSerAlaArgTyAsnLeuAlaAlaPheGlyPhePheGlyPhePheValTyAla 96
 Db 181 TGCTCTGCTCGTTACAACTTAGCAATTTTGGCTTTTGGCTTTTCTTCTTCTGATGCA 240
 QY 97 LeuArgValAsnLeuSerValAlaLeuValAspMetValAspSerAsnThrThrLeuGlu 116
 Db 241 TTACGTGTGAATCTCAGGTGTTCGGTGTAGGTATGGTATGTTCAATACAACTTTAGAA 300
 QY 117 AspAsnArgThrSerLysAlaCysProGluHisSerAlaProIleLysValHisAsn 136
 Db 301 GATAATAGAACTTCAAGGGCGTTCAGAGCAATCTGCTCCCAATAAAGTTTCATCAAT 360
 QY 137 GlnThrGlyLysLysGlyGlnThrAspAlaGluThrGlnGlyThrIleLeuGlySerPhe 156
 Db 361 CAAACGGGTAAAGATCAACCAATGGGATGAGAACTCAAGGATGATTCGCGTTCCTTT 420
 QY 157 PheTyGlyTyIleIleIleThrGlnIleProGlyGlyTyValAlaSerLysIleGlyGly 176
 Db 421 TTTTATGCTACATCATCACAGATCTCTGAGGATATGTTGCCAGCAAAATAGGGGG 480
 QY 177 LysMetLeuLeuGlyPheGlyIleLeuGlyThrAlaValLeuThrLeuPheThrProIle 196
 Db 481 AAAATGCTGTAGGATTTGGGATCTTGGCACTGTCTGCTCCACCTGTCTCACTCCCAT 540
 QY 197 AlaAlaAspLeuGlyValGlyProLeuIleValLeuArgAlaLeuGlyGlyLeuGlyGlu 216
 Db 541 GCTGCAGATTTAGGAGTTGGACCACTCATTTGACTCAGAGCACTAGAGAGCTAGGAG 600
 QY 217 GlyValThrPheProAlaMetHisAlaMetTrpSerSerTrpAlaProLeuGluArg 236
 Db 601 GGTGTTCATTTCCAGCAGCATGCCATGTGGTCTTCTTGGGCTCCCTCTTGAAGA 660
 QY 237 SerLysLeuLeuSerIleSerTyAlaGlyAlaGlnLeuGlyThrValIleSerLeuPro 256
 Db 661 AGCAAACTTCTTAGCATTTTCATATGCAGGAGCACAGCTTGGGACAGTAATTTCTCTCT 720
 QY 257 LeuSerGlyIleIleCysTyTrpMetAsnTrpThrTyValPheTyPhePheGlyThr 276
 Db 721 CTTTCTGGAATAAATTTGCTACTATATGAATTTGGACTATGTCTTCTTCTTCTTGTACT 780
 QY 277 IleGlyIlePheThrPheLeuLeuTrpIleTrpLeuValSerAspThrProGlnLysHis 296
 Db 781 ATTGGAATAATTTGTTTCTTTTGTGGATCTGGTATGTAGTGTAGTGTAGTGTAGTGTAGT 840

QY 297 LysArgIleSerHisTyTrpGlyGlyGluTyTrpIleLeuSerSerLeuArgAsnGlnLeuSer 316
 Db 841 AAGAGAATTTCCCATTTATGAAAAGGAATACATCTTTTCATCATTAAGAAATCAGCTTTCT 900
 QY 317 SerGlnLysSerValProTrpValProIleLeuLysSerLeuProLeuTrpAlaIleVal 336
 Db 901 TCAGAGAAAGTCAGTCCGCTGGGTACCCATTTTAAATCCCTGGCCACTTTGGGCTATCGTA 960
 QY 337 ValAlaHisPheSerTyAsnTrpThrPheTyTrpLeuLeuThrLeuLeuProThrTyTrp 356
 Db 961 GTTGACACATTTTCTTACAACTGGACTTTTATATCTTATTTGACATATTTGGCTACTTAT 1020
 QY 357 MetLysGluIleLeuArgPheAsnValGlnGluAsnGlyPheLeuSerSerLeuProTyTrp 376
 Db 1021 ATGAAGGAGATCCTAAGGTTCAATGTTCAAGAGAATGGGTTTTATCTTCATTTGCTTAT 1080
 QY 377 LeuGlySerTrpLeuCysMetIleLeuSerGlyGlnAlaAlaAspAsnLeuArgAlaLys 396
 Db 1081 TTAGGCTCTTGGTTATGTATGATCTGTCTGGTCAAGCTGTGCAATTTAAGGGCAAAA 1140
 QY 397 TrpAsnPheSerThrLeuCysValArgArgIlePheSerLeuIleGlyMetIleGlyPro 416
 Db 1141 TGGAAATTTTCACTTTATGTGTCGAGAAATTTTACGCTTATAGCAATGATTTGGACT 1200
 QY 417 AlaValPheLeuValAlaAlaGlyPheIleGlyCysAspTyTrpSerLeuAlaValAlaPhe 436
 Db 1201 GCAGTATTTCTGGTAGCTGTGGCTTCATTTGGCTGTGATTTCTTTGGCGGTTGCTTTC 1260
 QY 437 LeuThrIleSerThrThrLeuGlyGlyPheCysSerSerGlyPheSerIleAsnHisLeu 456
 Db 1261 CTAACTATATCAACACACTGGGAGGCTTTTGTCTTCTTGGATTTAGCATCAACCATCTG 1320
 QY 457 AspIleAlaProSerTyAlaGlyIleLeuLeuGlyIleThrAsnThrPheAlaThrIle 476
 Db 1321 GATATTGCTCTTGTATGTCTGCTATCTCTCTGGGCATCAACAATACATTTGCCACTATT 1380
 QY 477 ProGlyMetValGlyProValIleAlaLysSerLeuThrProAspAsnThrValGlyGlu 496
 Db 1381 CCAGGAATGGTTGGGCGCTCATTTGCTAAAGTCTGACCCCTGATAACACTGTTGGAGAA 1440
 QY 497 TrpGlnThrValPheTyTrpIleAlaAlaIleAlaValPheGlyAlaIlePhePheThr 516
 Db 1441 TGGCAAAACCGTGTCTATATTGCTGTCTGCTATTAATGTTTGGTGCCATTTCTTTTACA 1500
 QY 517 LeuPheAlaLysGlyGluValGlnAsnTrpAlaLeuAsnAspHisHisGlyHisArgHis 536
 Db 1501 CTATTGCCAAAGTGAAGTACAAAACCTGGGCTCTCAATGATCACCATGGACACAGACAC 1560

RESULT 2
 AK029102 3202 bp mRNA linear HTC 03-APR-2004
 LOCUS Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
 DEFINITION library, clone:4732491M05 product:SIALIN homolog (Homo sapiens),
 full insert sequence.
 ACCESSION AK029102
 VERSION AK029102.1 GI:26325087
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Mech. Enzymol. 303, 19-44 (1999)
 99279253
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE
 JOURNAL
 TITLE
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

GenCore version 5.1.6
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Run on: July 9, 2005, 07:16:14 ; Search time 910.316 Seconds
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Title: US-09-776-865-2

Perfect score: 2836

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Searched: 6330943 seqs, 3139157217 residues

Total number of hits satisfying chosen parameters: 12661886

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

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4	2804	98.9	3362	10	US-09-814-353-19097	Sequence 19097, A
5	2770.5	97.7	3329	19	US-10-755-889-587	Sequence 587, App
6	2761	97.4	3292	21	US-10-887-553A-858	Sequence 858, App
7	2717	95.8	2602	21	US-10-823-506-1	Sequence 1, Appli
8	2614	92.2	1488	13	US-10-098-841-322	Sequence 322, App
9	2338	82.4	2844	9	US-09-776-865-3	Sequence 3, Appli
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ALIGNMENTS

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; Patent No. US20020061846A1
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; APPLICANT: Hellergvist, Carl
; TITLE OF INVENTION: Methods for Preventing or Attenuating Pathoangiogenic Conditions
; FILE REFERENCE: 22100-0100 46126-252687
; CURRENT APPLICATION NUMBER: US/09/776,865
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,870
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2930

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US-09-776-865-1

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; Publication No. US20050002931A1
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; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/0105
; CURRENT APPLICATION NUMBER: US/10/823,506
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/359,167
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-693,843
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 2930
; TYPE: DNA
; ORGANISM: Homo sapiens
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Perfect score: 2836

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4	2338	82.4	2844	4	US-09-359-167-3
5	2217	78.2	1485	4	US-09-359-167-9
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7	956	33.7	1811	4	US-09-740-041-1
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20	795	28.0	1229	4	US-08-023-655-660	Sequence 660, App
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ALIGNMENTS

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; Patent No. 6803448
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/01US
; CURRENT APPLICATION NUMBER: US/09/359,167
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 60-693,843
; EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2930
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)..(1870)
US-09-359-167-7

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Score: 2836.00 Matches: 536
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-776-865-2 (1-536) x US-09-359-167-7 (1-2930)

Qy 1 MetAlaAlaClyAlaMetThrProProArgProValGlnProAlaArgProGlyGlyPhe 20

Db 263 ATGGGGGGGGGGGATGACACCGCCCGCGGTCCAGCCAGCTCGCGCGGGGGCTTC 322
Qy 21 GlyLeuSerGlyArgArgSerLeuLeuCysGlnValAlaSerThrProAlaHisValGly 40
Db 323 GGGCTGTGGCGGGCGCTCCCTCTCTGCCAGGTGGGAGTACACCTGCTCAGTAGGC 382
Qy 41 ValMetArgSerProValArgAspLeuAlaArgAsnAspGlyGluGluSerThrAspArg 60
Db 383 GTCATGAGGTCTCCGGTTCGAGACCTGGCCCGGAACGATGCGGAGGAGAGCAGCGACCGC 442
Qy 61 ThrProLeuLeuProGlyAlaProArgAlaGluAlaProValCysCysSerAlaArg 80
Db 443 ACGCTCTTTCACCGGGGGCGCCACGGGCCCAAGCGCTCCAGGTGTCTGCTCGT 502
Qy 81 TyrAsnLeuAlaLeuAlaPhePheGlyPhePheLeuValTyrAlaLeuArgValAsn 100
Db 503 TACAACCTAGCAATTTGGCTTTTGGTTCTTCATTGTGTATGCATTACGTGTGAAT 562
Qy 101 LeuSerValAlaLeuValAspMetValAspSerAsnThrThrLeuGluAspAsnArgThr 120
Db 563 CTGAGTGTGGGTAGTGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 622
Qy 121 SerLysAlaCysProGluHisSerAlaProLeuLysValHisAsnGlnThrGlyLys 140
Db 623 TCCAAGGGGTCTCAGAGCATCTGCTCCCAATAAAGTTTCATCAATCAAAACGGGTAA 682
Qy 141 LysTyrGlnTyrAspAlaGluThrGlnGlyTyrLeuGlySerPhePheTyrGlyTyr 160
Db 683 AAGTACCAANTGGATGCGAAGCTCAAGGATGGATTCTCGGTTCTCTTTTATGGCTAC 742
Qy 161 IleLeuThrGlnIleProGlyGlyTyrValAlaSerLysIleGlyLysMetLeuLeu 180
Db 743 ATCATCACACAGATCTCTGGAGGATATGTTGCCAGCAAAATAGGGGGGAAAATGCTGCTA 802
Qy 181 GlyPheGlyIleLeuGlyThrAlaValLeuThrLeuPheThrProIleAlaAlaAspLeu 200
Db 803 GGATTTGGGATTCCTTGGCACATGCTGCTCCACCTGTTCACTCCCATTTGCTGCAGATTA 862
Qy 201 GlyValGlyProLeuIleValLeuArgAlaLeuGluGlyLeuGlyGluValThrPhe 220
Db 863 CGAGTTGGACCACTCATTTGTTACTCAGACCATAGAGCACTAGAGAGGGGTTCATATT 922
Qy 221 ProAlaMetHisAlaMetTyrSerSerTrpAlaProProLeuGluArgSerLysLeuLeu 240
Db 923 CCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 982
Qy 241 SerIleSerTyrAlaGlyAlaGlnLeuGlyThrValIleSerLeuProLeuSerGlyIle 260
Db 983 AGCATTTTCGTATGCAGGAGCAGCTGGGACAGTAATTTCTCTCTCTTCTTCTGGAATA 1042
Qy 261 IleCysTyrTyrMetAsnTyrThrTyrValPheTyrPheGlyThrIleGlyIlePhe 280
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Qy 281 TrpPheLeuLeuTrpIleTrpLeuValSerAspThrProGlnLysHisLysArgIleSer 300
Db 1103 TGGTTCTTTTGTGATCTGTTAGTTAGTACACACACCAACCAACCAAGAGAATTTCC 1162
Qy 301 HisTyrGluLysGluTyrIleLeuSerSerLeuArgAsnGlnLeuSerSerGlnLysSer 320
Db 1163 CATTATGAAAGGAATAATATTTCTTCATCATTAAGAAATCAGCTTTCTTCAAGAGTCA 1222
Qy 321 ValProTyrValProIleLeuLysSerLeuProLeuTrpAlaIleValValAlaHisPhe 340
Db 1223 GTGCGTGGGTACCAATTTTAAATCCCTGCACTTTTGGGCTATGCTAGTTGGACATTT 1282
Qy 341 SerTyrAsnTyrThrPheTyrThrLeuLeuThrLeuLeuProThrTyrMetLysGluIle 360
Db 1283 TCTTACAACCTGGACTTTTATCTTATATGACATTTATGCTCTCTCTCTCTCTCTCTCT 1342
Qy 361 LeuArgPheAsnValGlnGluAsnGlyPheLeuSerSerLeuProTyrLeuGlySerTrp 380
Db 1343 CTAAGGTTCAATGTTCAAGAGATGGGTTTTTATCTCTCTCTCTCTCTCTCTCTCTCTCT 1402

Qy 381 LeuCysMetIleLeuSerGlyGlnAlaAlaAspAsnLeuArgAlaLysTyrAsnPheSer 400
Db 1403 TTAATGATGATCTGCTGCTCAAGCTGCTGCAAAATTAAGGGCAAAATGGAATTTTCA 1462
Qy 401 ThrLeuCysValArgArgIlePheSerLeuIleGlyMetIleGlyProAlaValPheLeu 420
Db 1463 ACTTTATGTCTTCGCAAAATTTTATAGCTTATAGGAATGATGGACCTGAGTATTCCTG 1522
Qy 421 ValAlaAlaGlyPheIleGlyCysAspTyrSerLeuAlaValAlaPheLeuThrIleSer 440
Db 1523 GTAGCTGCTGGCTTCATGCTGCTGATATTCTTTGGCCGTTGCTTCTTAATACTATCA 1582
Qy 441 ThrThrLeuGlyGlyPheCysSerSerGlyPheSerIleAsnHisLeuAspIleAlaPro 460
Db 1583 ACAACCTGGAGGCTTTTCTCTCTGATTTAGCATCAACCATCTGGATATTGCTCTCT 1642
Qy 461 SerTyrAlaGlyIleLeuLeuGlyIleThrAsnThrPheAlaThrIleProGlyMetVal 480
Db 1643 TCGTATGCTGGTATCTCTCTGGCATCAAAATACATTTTCCCATTAATTCAGGAATGTT 1702
Qy 481 GlyProValIleAlaLysSerLeuThrProAspAsnThrValGlyGluTyrGlnThrVal 500
Db 1703 GGGCCCGCTCATTTGCTAAAGTCTGACCCCTGATAACACTGTTGGAGATGGCAACCGTG 1762
Qy 501 PheTyrIleAlaAlaAlaIleAsnValPheGlyValaIlePhePheThrLeuPheAlaLys 520
Db 1763 TTTCTATATTGCTGCTGCTATTAATGTTTTTGGTGCCATTTTCTTACACTATTTCGCCAAA 1822
Qy 521 GlyGluValGlnAsnTrpAlaLeuAsnAspHisHisGlyHisArgHis 536
Db 1823 GGTGAAGTACAAAACCTGGGCTCTCAATGATCACCATGGACACAGACAC 1870

RESULT 2

US-09-949-016-1834
; Sequence 1834, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1834
; LENGTH: 2513
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1834

Alignment Scores:
Pred. No.: 6,62e-297 Length: 2513
Score: 2804.50 Matches: 534
Percent Similarity: 96.05% Conservative: 1
Best Local Similarity: 95.87% Mismatches: 1
Query Match: 98.89% Indels: 21
DB: 4 Gaps: 1

US-09-776-865-2 (1-536) x US-09-949-016-1834 (1-2513)

Qy 1 MetAlaAlaGlyAlaMetThr-----
Db 86 ATGGCGCGGGGGCGGAGTGGCGCGCGCGCTTGGCGGGGACCGGGGACTAGACGT 145
Qy 8 -----ProArgProValGlnProAlaArgProGlyGly 19

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2005, 02:43:23 ; Search time 803.74 Seconds
(without alignments)
3947.771 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 2836

Sequence: 1 MAAGATPPRPVQPARPGF.....LFAKEVQWALNDHGHHRH 536

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO_spool/US09776865/runat 08072005 175548 23365/app query.fasta_1.1358
-DB=N Geneseq 16Dec04 -QFMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09776865 @CGN 1 1 1004 @runat 08072005 175548 23365 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 16Dec04.*

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3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
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8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004as.*
13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2836	100.0	2930	3 AAZ50879	Aaz50879 Full leng
2	2836	100.0	2930	4 AAD10325	Aad10325 Human gro
3	2804.5	98.9	2511	12 ADQ84158	Adq84158 Human tum
4	2804	98.9	2512	4 AAF55900	Aaf55900 Human AST
5	2804	98.9	2626	11 ACN91332	Acn91332 Breast ca

6	2804	98.9	3362	5 ADL45207	Adl45207 Human ova
7	2770.5	97.7	3329	12 ADJ75057	Adj75057 Marker ge
8	2770.5	97.7	3329	13 ADRI4586	Adri4586 Human NF-
9	2770.5	97.7	3329	13 ADP25216	Adp25216 PRO poly
10	2734	96.4	2712	4 AAK94876	Aak94876 Human ful
11	2734	96.4	2712	12 ADL32035	Adl32035 Full leng
12	2717	95.8	2602	3 AAZ50875	Aaz50875 Partial h
13	2614	92.2	1488	4 AAI58115	Aai58115 Human pol
14	2338	82.4	2844	3 AAZ50876	Aaz50876 Sheep gro
15	2338	82.4	2844	4 AAD10326	Aad10326 Sheep gro
16	2217	78.2	1485	3 AAZ50880	Aaz50880 Human/She
17	1967	69.4	1485	3 AAZ50881	Aaz50881 Human/She
18	1716	60.5	2670	4 AAH79234	Aah79234 Human sod
19	1614	56.9	929	4 AAI59901	Aai59901 Human pol
20	1521	53.6	1872	6 ABO54422	Abg54422 Human ova
21	1515	53.4	1651	6 ABL90384	Abi90384 Human pol
22	1417	50.0	853	4 AAK93901	Aak93901 Human con
23	1417	50.0	853	12 ADL30328	Adl30328 3' end of
24	1339.5	47.2	838	4 AAK92364	Aak92364 Human cDN
25	1339.5	47.2	838	12 ADL48791	Adl28791 5' end of
26	996.5	35.1	1939	4 ABL03769	Abi03769 Drosophil
27	992	35.0	1641	4 ABL18113	Abi18113 Drosophil
28	992	35.0	1786	4 ABL07417	Abi07417 Drosophil
29	984.5	34.7	4899	4 ABL03768	Abi03768 Drosophil
30	973	34.3	3982	8 ABX13554	Abx13554 Rat DNPI
31	973	34.3	3982	9 ACF23330	Acf23330 Rat Na-de
32	973	34.3	3982	10 ADC15491	Adc15491 Rat DNPI
33	971	34.2	2528	8 ABX13555	Abx13555 Murine DN
34	971	34.2	2528	10 ADC15493	Adc15493 Mouse DNP
35	968	34.1	3946	8 ABX13553	Abx13553 Human DNP
36	968	34.1	3946	10 ADC15489	Adc15489 Human DNP
37	962	33.9	3422	4 AAK52406	Aak52406 Human pol
38	956	33.7	1811	6 ABK87049	Abk87049 Human tra
39	956	33.7	1811	10 ADG88328	Adg88328 Human tra
40	955	33.7	1767	10 ADD01393	Add01393 Human TCH
41	955	33.7	1850	10 ADD01409	Add01409 Human TCH
42	955	33.7	3671	9 AAL62505	Aal62505 Human tra
43	955	33.7	3952	13 ADR08065	Adr08065 Full leng
44	945	33.3	1803	10 ADD01411	Add01411 Mouse TCH
45	945	33.3	1822	10 ADD01422	Add01422 Mouse TCH

ALIGNMENTS

RESULT 1

AAZ50879
ID AAZ50879 standard; cDNA; 2930 BP.

XX AAZ50879;

XX 31-MAY-2000 (first entry)

XX Full length human GBS toxin receptor (HP59) cDNA.

XX Human GBS toxin receptor; group B beta-haemolytic streptococci; HP59;
XX pathological vascularisation; cancer metastases; angiogenesis;
XX neovascularisation; reperfusion injury; scarring; keloid;
XX chronic inflammation; rheumatoid arthritis; psoriasis; neural injury;
XX endothelial cell proliferation; antibacterial; anticancer;
XX anti-angiogenic; anti-inflammatory; anti-arthritis; anti-psoriatic; ss.
XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 263..1873

XX FT /**tag= a

XX FT /product= "Human GBS toxin receptor protein"

XX WO200005375-A1.

XX 03-FEB-2000.

XX 22-JUL-1999; 99WO-US016676.

XX 22-JUL-1998; 98US-0093843P.
XX (UYVA-) UNIV VANDERBILT.
XX Helleqvist CG, Fu C;
XX WPI; 2000-205377/18.
DR P-PSDB; AAY45089.
XX New polynucleotide encoding mammalian receptor for streptococcus toxin,
PT useful for diagnosis and treatment of, e.g. pneumonia in neonates.
XX Claim 3; Page 89-93; 109pp; English.
XX The present cDNA sequence encodes full length human GBS (Group B beta -
CC haemolytic streptococci) toxin receptor (HP59). This sequence was cloned
CC by using human embryo lung cDNA library as template. Expression vectors
CC comprising this cDNA can be transformed into host cells to express GBS
CC toxin receptor and its fragments. Detecting the receptor in tissues is
CC used to diagnose pathological vascularisation, e.g. for detecting cancer
CC metastases. GBS toxin receptors are useful for treating conditions
CC associated with pathological angiogenesis or neovascularisation
CC (specifically cancer, reperfusion injury, scarring during wound healing,
CC keloids, chronic inflammation (rheumatoid arthritis or psoriasis) or
CC neural injury), and to raise specific antibodies used for treating early
CC onset disease. Inhibitors of this receptor are useful for treating
CC pathological or hypoxia-induced endothelial cell proliferation and
CC migration
XX
SQ Sequence 2930 BP; 729 A; 698 C; 681 G; 822 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.4e-264 Length: 2930
Score: 2836.00 Matches: 536
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-776-865-2 (1-536) x AAZ50879 (1-2930)

Qy 1 MetAlaAlaGlyAlaMetThrProArgProValGlnProAlaArgProGlyGlyPhe 20
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Qy 21 GlyLeuSerGlyArgSerLeuLeuCysGlnValAlaSerThrProAlaHisValGly 40
Db 323 GGGCTGTGCGGGCGGCGCTCCCTTCTCTGCCAGGTGGCGAGTACACCTGCTCAGTAGGC 382

Qy 41 ValMetArgSerProValArgAspLeuAlaArgAsnAspGlyGluGluSerThrAspArg 60
Db 383 GTCATAGGTCTCCGGTTCGAGACTGGCCCGGAGACGNTGGCGAGAGACGCGACCGC 442

Qy 61 ThrProLeuLeuProGlyAlaProArgAlaGluAlaProValCysCysSerAlaArg 80
Db 443 ACGGCTCTTACCGGGCGGCCACCGGCGGAGCGCTCCAGGTGCTGCTCTGCTCGT 502

Qy 81 TyrAsnLeuAlaLeuAlaPhePheGlyPhePheLeuValTyrAlaLeuArgValAsn 100
Db 503 TACAACCTTAGCAATTTTGGCCCTTTTGGTTCTTTCATTGTGTATGCAATACGTTGAAT 562

Qy 101 LeuSerValAlaLeuValAspMetValAspSerAsnThrThrLeuGluAspAsnArgThr 120
Db 563 CTGAGTGTGGGTAGTGATATGATGATGATGATGATGATGATGATGATGATGATGAT 622

Qy 121 SerLysAlaCysProGluHisSerAlaProLeuLysValHisHisAsnGlnThrGlyLys 140
Db 623 TCCAAGGGGTGCCAGAGCATTCGCTCCCAAAAAGTTTCATCATAATCAAAACGGTAAG 682

Qy 141 LysTyrGlnTrpAspAlaGluThrGlnGlyTrpLeuLeuGlySerPhePheTyrGlyTyr 160
Db 683 AAGTACCAATGGGATGCGAGAAACCAAGGATGGATTTCTCGGTTCCTTTTATGGGTAC 742

Qy 161 IleIleThrGlnIleProGlyGlyTyrValAlaSerLysIleGlyGlyLysMetLeuLeu 180
Db 743 ATCATCACAGATTCTCGGAGGATATGTTGCCAGCAAAATAGGGGGGAAAATGCTCTCTA 802

Qy 181 GlyPheGlyIleLeuGlyThrAlaValLeuThrLeuPheThrProIleAlaAlaAspLeu 200
Db 803 GGATTTGGGATCTCTGGCACTGCTGTCTCCTCACCTGTTCACCTCCCATTTGTCGAGATT 862

Qy 201 GlyValGlyProLeuIleValLeuArgAlaLeuGluGlyLeuGlyGluGlyValThrPhe 220
Db 863 GGAGTTGGACCATCATTTGTTACTCAGAGCACTAGAGGACTAGAGAGGGGTGTACATTT 922

Qy 221 ProAlaMetHisAlaMetTrpSerSerTrpAlaProProLeuGluArgSerLysLeuLeu 240
Db 923 CAGCCATGATGCCATGTGCTCTCTTGGCTCCCTCTTGAAGAAGCAAAATCTCTT 982

Qy 241 SerIleSerTyrAlaGlyAlaGlnLeuGlyThrValIleSerLeuProLeuSerGlyIle 260
Db 983 AGCATTTGCTATGCGAGGACGACGCTTGGGACAGTAATTTCTCTCTCTCTCTCTCTCT 1042

Qy 261 IleCysTyrTyrMetAsnTrpThrTyrValPheTyrPhePheGlyThrIleGlyIlePhe 280
Db 1043 ATTTGCTACTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1102

Qy 281 TrpPheLeuLeuTrpIleTrpLeuValSerAspThrProGlnLysHisLysArgIleSer 300
Db 1103 TGGTTTCTTTTGTGGATCTGTTAGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 1162

Qy 301 HisTyrGluLysGluTyrIleLeuSerSerLeuArgAsnGlnLeuSerSerGlnLysSer 320
Db 1163 CATTATGAAAAGGAATACATTTCTTATCAATTAAGAAATCAGCTTTCTTCCACAGAGTCA 1222

Qy 321 ValProTrpValProIleLeuLysSerLeuProLeuTrpAlaIleValValAlaHisPhe 340
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Qy 341 SerTyrAsnTrpThrPheTyrThrLeuLeuThrLeuLeuProThrTyrMetLysGluIle 360
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Qy 361 LeuArgPheAsnValGlnGluAsnGlyPheLeuSerSerLeuProTyrLeuGlySerTrp 380
Db 1343 CTAAGGTTCATATGTTCAAGAGAAATGGGTTTTATCTTATCTTATTTAGGCTCTTTG 1402

Qy 381 LeuCysMetIleLeuSerGlyGlnAlaAlaAspAsnLeuArgAlaLysTrpAsnPheSer 400
Db 1403 TTATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1462

Qy 401 ThrLeuCysValArgArgIlePheSerLeuIleGlyMetIleGlyProAlaValPheLeu 420
Db 1463 ACTTTATGTTTCGAGAAATTTTATAGCTTATAGGAATGATGGACCTGCAGTATTCTCT 1522

Qy 421 ValAlaAlaGlyPheIleGlyCysAspTyrSerLeuAlaValAlaPheLeuThrIleSer 440
Db 1523 GTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582

Qy 441 ThrThrLeuGlyGlyPheCysSerSerGlyPheSerIleAsnHisLeuAspIleAlaPro 460
Db 1583 ACAACACTGGAGGCTTTTGTCTCTTGGATTTTAGCATCAACCATCTGGATATTGCTCT 1642

Qy 461 SerTyrAlaGlyIleLeuLeuGlyIleThrAsnThrPheAlaThrIleProGlyMetVal 480
Db 1643 TCGTATGCTGGTATCT 1702

Qy 481 GlyProValIleAlaLysSerLeuThrProAspAsnThrValGlyGluTrpGlnThrVal 500
Db 1703 GGCGCCGCTCATTTGCTAAAGCTGACCCCTGAAACACTGTTGGAGAAATGGCAACCGTG 1762

Qy 501 PheTyrIleAlaAlaAlaIleAsnValPheGlyAlaIlePhePheThrLeuPheAlaLys 520
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Result No.	Score	Query Match	Length	DB	ID	Description
1	2836	100.0	2930	6	BD248129	BD248129 GBS toxin
2	2836	100.0	2930	6	AX207624	AX207624 Sequence
3	2836	100.0	2930	9	AF244577	AF244577 Homo sapi
4	2804	98.9	2512	6	AX138494	AX138494 Sequence

PF 22-JUL-1999 JP 2000561321
PR 22-JUL-1998 US 60/093843
PI CARL G HELLERQVIST, CHANGLIN
PC C12N15/09, A61K45/00, A61P9/00,
A61P35/00,
PC A61P43/00, C07K14/705, C07K16
C12N5/10,
PC C12P21/02, C12Q1/02, G01N33/1
G8S toxin receptor

FEATURES	source	FH FT	Key CDS	Location/Qualifiers (263)..(1870).	Location/Qualifiers 1..2930 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
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Alignment Scores:					
Pred. No.:	6 5e-223			Length:	2930
Score:	2836.00			Matches:	536
Percent Similarity:	100.00%			Conservative:	0
Best Local Similarity:	100.00%			Mismatches:	0
Query Match:	100.00%			Indels:	0
DB:	6			Gaps:	0
US-09-776-865-2 (1-536) x BD248129 (1-2930)					
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Dd	263	ATGCGGGGGGGCGATGCACACGCCCGCCGGTCCAGCCAGCTCGCCCCGGGGGTTC	322		
Qy	21	GlyLeuSerGlyArgArgSerLeuLeuCysGlnValAlaSerThrProAlaHisValGly	40		
Dd	323	GGGCTGTGGGGCGCGCTCCTCTCTGCCAGGTGGCGAGTACACTGCTCACGTAGGC	382		
Qy	41	ValMetArgSerProValArgAspLeuAlaArgenAspGlyGluGluSerThraSparg	60		
Dd	383	GTCATGAGGTCTCGGTTCGAGACCTGGCCCCGAACGATGCGAGGAGCAGCACGCCG	442		
Qy	61	ThrProLeuLeuProGlyAlaProArgAlaGluAlaProValCysCyserAlaAarg	80		
Dd	443	ACGCTCTTCTACGGGGGGCCCCAGGGCCGAGCGGCTCAGTGTGTCTGTCTGCTCGT	502		
Qy	81	TyrAnLeuAlaIleLeuAlaPhePhedGlyPhePheIleValTyrAlaLeuArgValAsn	100		
Dd	503	TACAACATTAGCAATTTTGCCCTTTTTTGTTCTTCATTGTGTATGCATTACGTGTGAAT	562		
Qy	101	LeuSerValAlaLeuValAspMetValAspSerAsnThrThrLeuGluAspAsnArgThr	120		
Dd	563	CTGAGTGTGGGTTAGTGGATATGGTAGATTCAAATAACAATCTTAGAAGAATAAGAACT	622		
Qy	121	SerLysAlaCysProGluHisSerAlaProIleLysValHisHisAsnGlnThrGlyLys	140		
Dd	623	TCCNAGSGGTGCCAGAGCATTCGTCCCATAAAGTTCAATCATCAATCAAACGGGTAG	682		
Qy	141	LysTyrGlnTrpAspAlaGluThrGlnGlyTrpIleLeuGlySerPhePheTyrGlyTyr	160		
Dd	683	AAGTACCAATGGGATGCAGAACTCAAGGATGGATTCTCGGTTCCTTTTTTATGGCTAC	742		
Qy	161	IleIleThrGlnIleProGlyGlyTyrValAlaSerLysIleGlyGlyLysMetLeuLeu	180		
Dd	743	ATCATCACACAGATTCTCTGGAGGATATGTGCCAGCAAAATAGGGGGAAAATCTGCTGA	802		
Qy	181	GlyPheGlyIleLeuGlyThrAlaValLeuThrLeuPheThrProIleAlaAspLeu	200		
Dd	803	GGATTGGGATCCCTGGACATGCTCTCTACCCTTGTTCACTCCCATTTGCTGCAGATTTA	862		
Qy	201	GlyValGlyProLeuIleValLeuArgAlaLeuGluGlyLeuGlyGluGlyValThrPhe	220		
Dd	863	GGAGTTGGACCACATTTGTACTCAGAGCACTAGAAGGACTAGGAGAGGGTGTACATTT	922		
Qy	221	ProAlaMetHisAlaMetTrpSerSerTrpAlaProProLeuGluArgSerLysLeuLeu	240		
Dd	923	CCAGCCATGCATGCGCATGTGGTCTCTTTGGGCTCCCCCTCTTGAAGAAGCAAACTTCTT	982		
Qy	241	SerIleSerTyrAlaGlyAlaGlnLeuGlyThrValIleSerLeuProLeuSerClyIle	260		
Dd	983	AGCATTTTCGTATGCAGGAGCACAGCTTGGAGAGTAATTTCTTCCTCTTCTTCTGGAATA	1042		
Qy	261	IleCysTyrTyrMetAsnTrpThrTyrValPheTyrPhePheGlyThrIleGlyIlePhe	280		

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OM protein - protein search, using sw model

Run on: July 9, 2005, 05:13:45 ; Search time 106.106 seconds
(without alignments)
2388.931 Million cell updates/sec

Title: US-09-776-865-4
Perfect score: 2617
Sequence: 1 MKSPVSLAPSDGEGSDRT.....LFAKGEVQNWAIHQHNRN 495

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2617	100.0	495	1 S175_SHEEP	Q9mzd1 ovis aries
2	2329	89.0	495	1 S175_HUMAN	Q9nra2 homo sapien
3	2236	85.4	495	1 S175_MOUSE	Q8bn82 mus musculu
4	1058	40.4	544	2 Q7Q580	Q7q580 anopheles g
5	1006	38.4	476	2 Q7Q579	Q7q579 anopheles g
6	991.5	37.9	559	2 Q9VYG7	Q9vyg7 drosophila
7	985.5	37.7	502	2 Q3VDM0	Q9vdm0 drosophila
8	979	37.4	589	2 Q8NDX2	Q8ndx2 homo sapien
9	976	37.3	588	2 Q8KIQ1	Q8kiq1 rattus norv
10	976	37.3	588	2 Q7TSF2	Q7tsf2 rattus norv
11	969.5	37.0	601	2 Q8BFU8	Q8bfu8 mus musculu
12	968.5	37.0	493	1 YLD2 CAEEL	Q03567 caenorhabdi
13	965	36.9	582	2 Q920B7	Q920b7 mus musculu
14	965	36.9	582	2 Q8J1I2	Q8j1i2 rattus norv
15	962.5	36.8	582	2 Q9P2U8	Q9p2u8 homo sapien
16	960	36.7	582	2 Q8BLE7	Q8ble7 mus musculu
17	941	36.0	529	1 P1C0 DROME	Q9v7b5 drosophila
18	940.5	35.9	576	2 Q6INC8	Q6inc8 xenopus lae
19	940	35.9	584	2 Q8AW47	Q8aw47 brachydanio
20	936	35.8	479	2 Q23514	Q23514 caenorhabdi
21	932	35.6	560	2 Q9P2U7	Q9p2u7 homo sapien
22	927	35.4	560	2 Q62634	Q62634 rattus norv
23	926	35.4	483	1 P1C0 DROAN	Q61369 drosophila
24	923	35.3	560	2 Q6PCD0	Q6pcd0 homo sapien
25	899.5	34.4	576	2 Q715L3	Q715l3 xenopus lae
26	884	33.8	466	2 Q96LH1	Q96lh1 homo sapien
27	881	33.7	955	2 Q932C5	Q932c5 anopheles g
28	874.5	33.4	497	2 Q7P2C5	Q7p2c5 homo sapien
29	860	32.9	535	2 Q7PWK4	Q7pwk4 anopheles g
30	859.5	32.8	481	2 Q9VJW8	Q9vjw8 drosophila
31	849.5	32.5	533	2 Q7Q1S5	Q7qls5 anopheles g

32	847.5	32.4	453	2	Q9NKF8	Q9nkf8 drosophila
33	845	32.3	479	2	Q9W4C7	Q9w4c7 drosophila
34	841.5	32.2	498	2	Q8CJH9	Q8cjh9 rattus norv
35	835.5	31.9	496	2	Q9VKC9	Q9vkc9 drosophila
36	833.5	31.8	470	2	Q7YTZ7	Q7ytz7 drosophila
37	819	31.3	563	2	Q9TZN7	Q9tzn7 caenorhabdi
38	819	31.3	576	1	YQO6 CAEEL	P34644 caenorhabdi
39	812.5	31.0	485	2	Q7PSC6	Q7psc6 anopheles g
40	809.5	30.9	465	1	NPT1_RABIT	Q28722 o renal sod
41	807.5	30.9	465	2	Q91WV5	Q91wv5 mus musculu
42	806.5	30.8	498	2	Q8VCY5	Q8vcy5 mus musculu
43	804.5	30.7	467	2	Q7YQJ7	Q7yqj7 sus scrofa
44	803	30.7	447	2	Q8VCX8	Q8vcx8 mus musculu
45	802.5	30.7	465	1	NPT1_MOUSE	Q61983 mus musculu

ALIGNMENTS

RESULT 1

S175_SHEEP STANDARD; PRT; 495 AA.
AC Q9WZD1;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sialin (Solute carrier family 17 member 5) (Sodium/sialic acid cotransporter) (Membrane glycoprotein SP55).
GN Name=SLC17A5;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Lung;
RX PubMed=11751519;
RA Fu C., Bhardhan S., Cetateanu N.D., Wamil B.D., Wang Y., Yan H.-P., Shi E., Carter C., Venkov C., Yakes F.M., Page D.L., Lloyd R.S., Mernaugh R.L., Hellerqvist C.G.;
RT "Identification of a novel membrane protein, HP59, with therapeutic potential as a target of tumor angiogenesis.";
RL Clin. Cancer Res. 7:4182-4194(2001).
CC FUNCTION: Primary solute translocator for anionic substances; particularly it is a free sialic acid transporter in the lysosomes (Probable). Receptor for CM101, a polysaccharide produced by group B Streptococcus with antipathoangiogenic properties.
CC B Streptococcus with antipathoangiogenic properties.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal (Potential).
CC -!- TISSUE SPECIFICITY: Significantly expressed in lung endothelial cells, and much less in liver.
CC -!- SIMILARITY: Belongs to the major facilitator (MFS) superfamily. Sodium/anion cotransporter family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF244578; AAF97770.1; -;
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub transporter.
DR Pfam; PF00083; Sugar tr; 1.
DR PROSITE; PSS0850; MFS; 1.
DR TRANSMEM 42 62
KW Lysosome; Receptor; Symport; Transmembrane; Transport.
FT TRANSMEM 110 130 Potential.
FT TRANSMEM 137 157 Potential.
FT TRANSMEM 159 179 Potential.

FT TRANSMEM 201 221 Potential.
FT TRANSMEM 228 248 Potential.
FT TRANSMEM 289 309 Potential.
FT TRANSMEM 329 349 Potential.
FT TRANSMEM 366 386 Potential.
FT TRANSMEM 392 412 Potential.
FT TRANSMEM 424 444 Potential.
FT TRANSMEM 458 478 Potential.
SQ SEQUENCE 495 AA; 54536 MW; 649D7C4A59B28272 CRC64;

Query Match 100.0%; Score 2617; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.8e-183;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPVSLAPSDGEGSDRTLLQAPRAEPAPCCSARYNLAFSPFPFVLSLRLNL 60
DB 1 MKSPVSLAPSDGEGSDRTLLQAPRAEPAPCCSARYNLAFSPFPFVLSLRLNL 60
QY 61 SVALVDMVDSNTAKDNRTSYECAPHSAP1KVLHNQTKGKYRDAETQGWILGSFFYGYI 120
DB 61 SVALVDMVDSNTAKDNRTSYECAPHSAP1KVLHNQTKGKYRDAETQGWILGSFFYGYI 120
QY 121 ITQIPGGVVASRSGKLLGFGIFATAIPTFTPLAADFGVGVALVALRALGEGGVTP 180
DB 121 ITQIPGGVVASRSGKLLGFGIFATAIPTFTPLAADFGVGVALVALRALGEGGVTP 180
QY 181 AHMAWSSWAPLERSKLLSISYAGAQLGTVVSLPSGVICYNNWTYVFFFGIVGLI 240
DB 181 AHMAWSSWAPLERSKLLSISYAGAQLGTVVSLPSGVICYNNWTYVFFFGIVGLI 240
QY 241 FILMTCVSDTPETHKTTIPYEKEYILSSLNQLSSQKSPWIPMLKSLPLWAIWVAFHS 300
DB 241 FILMTCVSDTPETHKTTIPYEKEYILSSLNQLSSQKSPWIPMLKSLPLWAIWVAFHS 300
QY 301 YNWTFTYLLTPTMYKVLRFNTQENGFLSAVPYLGWLCWILSGQADNLRWNPST 360
DB 301 YNWTFTYLLTPTMYKVLRFNTQENGFLSAVPYLGWLCWILSGQADNLRWNPST 360
QY 361 LWVRVFLSLIGMIGPAIFLVAAGFTGCDYSLAVAFITSTTLTGFCSSGFSINHLDIAPS 420
DB 361 LWVRVFLSLIGMIGPAIFLVAAGFTGCDYSLAVAFITSTTLTGFCSSGFSINHLDIAPS 420
QY 421 YAGILLGTTNTFATIPGMIGPIIARSLTPENTIGEWQTVFCIAAIVNFGAIFTFLPAKG 480
DB 421 YAGILLGTTNTFATIPGMIGPIIARSLTPENTIGEWQTVFCIAAIVNFGAIFTFLPAKG 480
QY 481 EVQNWAI5DHQHRN 495
DB 481 EVQNWAI5DHQHRN 495

RESULT 2

SI175_HUMAN STANDARD; PRT; 495 AA.
AC Q9NRA2; Q9NBR5; Q9UGH0;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sialin (Solute carrier family 17 member 5) (Sodium/sialic acid cotransporter) (AST) (Membrane glycoprotein HP59).
GN Name=SLC17A5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=11751519;
RA Fu C., Bardhan S., Cetateanu N.D., Wamil B.D., Wang Y., Yan H.-P., Shi E., Carter C., Venkov C., Yates F.M., Page D.L., Lloyd R.S., Mernaugh R.L., Hellerqvist C.G.;
RA "Identification of a novel membrane protein, HP59, with therapeutic potential as a target of tumor angiogenesis.";
RT

RL Clin. Cancer Res. 7:4182-4194 (2001).
RP [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, TISSUE SPECIFICITY, VARIANT SD CYS-39, AND VARIANTS ISSD 268-SER--ASN-272 DEL; ARG-183 AND ARG-334.
RX MEDLINE=20047778; PubMed=10581036; DOI=10.1038/70585;
RA Verheijen F.W., Verbeek E., Aula N., Beerens C.E.M.T., Havelaar A.C., Joosse M., Peltonen L., Aula P., Galjaard H., Van der Spek P.J., Mancini G.M.S.;
RA "A new gene, encoding an anion transporter, is mutated in sialic acid storage diseases.";
RT Nat. Genet. 23:462-465 (1999).
RL [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Ohayashi K., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuna M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Muesashino K., Yuuki H., Oshima A., Sasaki N., Aoeuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Motiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani K., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RP "Complete sequencing and characterization of 21,243 full-length human cDNAs.";
RL Nat. Genet. 36:40-45 (2004).
RP [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP [5]
RP VARIANTS SD CYS-39 AND GLU-136, AND VARIANTS ISSD 268-SER--ASN-272 DEL; ARG-183; ARG-334 AND VAL-371.

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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:16:27 ; Search time 24.9661 Seconds
(without alignments)
1907.682 Million cell updates/sec

Title: US-09-776-865-4
Perfect score: 2617
Sequence: 1 MKSPVSLAPSDGEGSDRT.....LPKAGEVQNWAI SDHQGHRN 495

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	968.5	37.0	493	2 G88553	protein C38C10.2 [
2	950	36.3	472	2 S28286	hypothetical prote
3	927	35.4	560	2 I59302	brain specific Na+
4	819	31.3	563	2 T43650	probable sodium-de
5	819	31.3	576	2 H88548	protein ZK512.6 [i
6	809.5	30.9	465	2 A56410	sodium/phosphate t
7	802.5	30.7	465	2 S59915	sodium-phosphate t
8	792.5	30.3	573	2 T23589	hypothetical prote
9	791.5	30.2	467	2 A48916	sodium phosphate t
10	775.5	29.6	465	2 I39473	Na+-dependent phos
11	766.5	29.3	544	2 T24633	hypothetical prote
12	744	28.4	512	2 H84698	hypothetical prote
13	585	22.4	501	2 B89135	protein F25G6.7 [i
14	561.5	21.5	413	2 T01534	hypothetical prote
15	550.5	21.0	537	2 T45634	hypothetical prote
16	541.5	20.7	466	2 S40767	hypothetical prote
17	499	19.1	561	2 D84800	hypothetical prote
18	490.5	18.7	592	2 T25419	hypothetical prote
19	489	18.7	568	2 S44742	C02C2.4 protein -
20	471	18.0	530	2 T29418	hypothetical prote
21	450	17.2	380	2 T29248	hypothetical prote
22	444.5	17.0	516	2 T24729	hypothetical prote
23	428	16.4	499	2 T15201	hypothetical prote
24	420	16.0	506	2 T29688	hypothetical prote
25	419.5	16.0	543	2 T23246	hypothetical prote
26	395.5	15.1	493	2 T25357	hypothetical prote
27	391.5	15.0	445	2 T23590	hypothetical prote
28	382.5	14.6	425	2 A90055	hypothetical prote
29	379.5	14.5	473	2 T31717	hypothetical prote

30	373	14.3	455	1	H69752	probable glucarat
31	371	14.2	485	2	T24115	hypothetical prote
32	369	14.1	452	2	A50861	probable glucarat
33	368.5	14.1	478	2	T33942	hypothetical prote
34	366.5	14.0	462	2	T34365	hypothetical prote
35	365.5	14.0	420	2	S44900	ZK652.10 protein -
36	361	13.8	450	2	A65061	probable glucarat
37	358.5	13.7	428	2	D0675	membrane transport
38	357	13.6	450	2	C85930	probable transport
39	357	13.6	450	2	A91085	probable transport
40	346.5	13.2	455	2	T34366	hypothetical prote
41	339.5	13.0	659	2	T33557	hypothetical prote
42	338.5	12.9	422	1	A69853	hexuronate transpo
43	334.5	12.8	493	2	T19383	hypothetical prote
44	331.5	12.7	516	2	T27092	hypothetical prote
45	326	12.5	487	2	T23776	hypothetical prote

ALIGNMENTS

RESULT 1

G88553
protein C38C10.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G88553
R:anonymous, The C. elegans Sequencing Consortium.
S:Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G88553
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <SNO>
A:Cross-references: UNIPROT:Q03567; GB:chr_III; PIDN:CNA79549.1; PID:G3874873; GSPDB:GN01
C:Genetics:
A:Gene: C38C10.2
A:Map position: 3

Query Match	37.0%	Score	968.5	DB 2	Length	493			
Best Local Similarity	40.5%	Pred. No.	1.9e-69						
Matches	193	Conservative	89	Mismatches	179	Indels	15	Gaps	6
Qy	27	PRAPAPVCCSARYNLAFSLFFGFVLSRLVNSVALVDMVDSNTTAKDNRTSYECAEH	86						
Db	8	PRLVP-----STRFALSLVNFEGCLVTYMRNTMNSPAVVCNVNENKTDGTGVEKYSRCGE	62						
Qy	87	SAPIKVLHNTGKKYRWDATQGWILGSPFYGIITQIPGVYASRSGKULLLGGIFAT	146						
Db	63	MTPVESNSSVIG-EFMDWKOTTTGMVLSFFYGTGSIIGHLASRYGGRVFWFTIILGS	121						
Qy	147	AIETLFTPLAADFCVGLVALRALEGEGVTYPAMHAMSSWAPPLERSKLLSISVAGA	206						
Db	122	ALLTLNLPVAARTSEYALILRAAIGFQATFPAMHTMMSVWGPPLELSVLTGVTVAGA	181						
Qy	207	QLGTWVSLPSGVICY---MNTVYFFYFGIVGIIWFIWILCVLSDTPTETHKITTPYEK	263						
Db	182	QIGNVIVLPSGLFCYCEYFGDGGWPSFIYIIGVFGVLTAVWVYSSDKPATHRITPEEK	241						
Qy	264	EYILSSLKNQLSSQ-----KSVPIPMPLKSLPLMAIVVAHFSYNWTFYLLTLLPTMYKEV	319						
Db	242	QYIVTAVEASMGKDTGKVPSTPWIKILTSAPVACWAGHFAAGDWGAVTMLVSLPSFLKDV	301						
Qy	320	LRFNIQENGFLSAVPIYGCWILMSLQQAADNLARWNFSLTWVRVPSLIGMIGPAIFL	379						
Db	302	LGLNLSLGAVASIPYIAYFLAINAGVGLADTLRSKIGILSTLNTRRAAMLVALIGQGIFL	361						
Qy	380	VAAGFICDYS-LAVAFLLTISTLGGFCSCGFSINHLDIAPSYAGILLGINTTATTIPGM	438						
Db	362	VASGYCCGQDVLVIIITCGMAISGLQYAGVFVNYLEIAPFFSGTVMGTGNTISALAGI	421						

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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:22:07 ; Search time 106.586 Seconds

(without alignments)
1794.174 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 2617

Sequence: 1 MKSPVSLAPSDGREGSDRT.....LFAKGEVQNAISDHQGRN 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
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- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pap.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pap.*
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- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pap.*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2329	89.0	495	9	US-09-915-181A-7
4	2329	89.0	495	16	US-10-755-889-588
5	2329	89.0	495	17	US-10-823-506-2
6	2329	89.0	536	9	US-09-776-865-2
7	2329	89.0	536	17	US-10-823-506-8
8	1702	65.0	495	17	US-10-823-506-10
9	1702	65.0	495	17	US-10-823-506-12
10	1386	53.0	284	15	US-10-264-049-2477
11	1318	50.4	272	15	US-10-264-237-2351

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14	979	37.4	589	18	US-10-499-731-28	Sequence 28, Appli
15	969.5	37.0	601	18	US-10-499-731-46	Sequence 46, Appli
16	968.5	37.0	493	15	US-10-369-493-5834	Sequence 5834, Ap
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18	965	36.9	578	14	US-10-389-967-4	Sequence 4, Appli
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20	965	36.9	582	15	US-10-205-331-7	Sequence 7, Appli
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22	965	36.9	582	16	US-10-734-731-14	Sequence 14, Appli
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25	962.5	36.8	582	16	US-10-734-731-10	Sequence 10, Appli
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27	958	36.6	566	15	US-10-287-226-300	Sequence 300, App
28	956.5	36.5	850	9	US-09-915-181A-3	Sequence 3, Appli
29	932	35.6	560	16	US-10-734-731-2	Sequence 2, Appli
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37	927	35.4	560	16	US-10-734-731-6	Sequence 6, Appli
38	927	35.4	560	16	US-10-734-731-8	Sequence 8, Appli
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40	927	35.4	560	16	US-10-807-500-8	Sequence 8, Appli
41	927	35.4	560	17	US-10-877-818-4	Sequence 4, Appli
42	895	34.2	194	15	US-10-296-115-1200	Sequence 1200, Ap
43	819	31.3	563	9	US-09-915-181A-6	Sequence 6, Appli
44	819	31.3	576	14	US-10-014-079A-1	Sequence 1, Appli
45	819	31.3	576	15	US-10-369-493-5823	Sequence 5823, Ap

ALIGNMENTS

RESULT 1
US-09-776-865-4
; Sequence 4, Application US/09776865
; Patent No. US20020061846A1
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; TITLE OF INVENTION: Methods for Preventing or Attenuating Pathoangiogenic Conditions
; FILE REFERENCE: 22100-0100 46126-252687
; CURRENT APPLICATION NUMBER: US/09/776.865
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,870
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Ovis sp.
US-09-776-865-4

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Db 181 AMHAMSSWAPPLERSKLLSISYAGAQLGTVVSLPLSGVICYNNWTVVFFFGIVGLI 240
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; Sequence 4, Application US/10823506
; Publication No. US20050002931A1
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/0105
; CURRENT APPLICATION NUMBER: US/10/823,506
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/359,167
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-693,843
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Ovis sp.
US-10-823-506-4

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Db 181 AMHAMSSWAPPLERSKLLSISYAGAQLGTVVSLPLSGVICYNNWTVVFFFGIVGLI 240
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Db 241 FILMICLVSDTPETHKTIITPYEKEYIILSSLNQKSSQKSVPMIPMLKSLPLWAIWVAHFS 300
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Qy 361 LWRRVFSLIGMIGPAIFLVAAGFIGCDYSIAVAFITISTITLGGFCSSGFSINHLDIAPS 420
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Qy 481 EVQNWAISSDHQHRN 495
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RESULT 3
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; Sequence 7, Application US/09915181A
; Patent No. US20020098473A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMEAU, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-932610US
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-181A-7

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Matches 427; Conservative 39; Mismatches 29; Indels 0; Gaps 0;

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1702	65.0	495	4	US-09-359-167-10
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8	979	37.4	589	4	US-09-740-041-2
9	965	36.9	578	4	US-09-915-181A-4
10	965	36.9	582	4	US-09-915-181A-3
11	956.5	36.5	850	4	US-09-915-181A-3
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17	927	35.4	560	2	US-08-805-118-4
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19	927	35.4	560	4	US-09-915-181A-5
20	874.5	33.4	497	4	US-09-949-016-6616
21	819	31.3	563	4	US-09-915-181A-6
22	819	31.3	576	3	US-08-864-785-1
23	797.5	30.5	465	4	US-09-915-181A-8
24	791.5	30.2	467	2	US-08-805-118-3
25	791.5	30.2	467	3	US-09-391-958-3
26	777	29.7	480	2	US-08-724-394A-9
27	761	29.1	552	4	US-09-270-767-45540

28	672	25.7	436	4	US-09-949-016-11448	Sequence 11448, A
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31	603.5	23.1	401	3	US-09-391-958-1	Sequence 1, Appl
32	592.5	22.6	480	2	US-08-724-394A-11	Sequence 11, Appl
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38	365.5	14.0	455	4	US-09-489-039A-9942	Sequence 9942, Ap
39	365	13.9	439	3	US-09-172-952-14	Sequence 12, Appl
40	365	13.9	439	4	US-09-922-501-12	Sequence 12, Appl
41	360	13.8	157	4	US-09-270-767-61037	Sequence 61037, A
42	353	13.5	434	4	US-09-489-039A-13633	Sequence 13633, A
43	341	13.0	163	4	US-09-270-767-32926	Sequence 32926, A
44	341	13.0	163	4	US-09-270-767-48143	Sequence 48143, A
45	326.5	12.5	459	4	US-09-489-039A-10630	Sequence 10630, A

ALIGNMENTS

RESULT 1
US-09-359-167-4
; Sequence 4, Application US/09359167
; Patent No. 6803448
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/01US
; CURRENT APPLICATION NUMBER: US/09/359,167
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 60-693,843
; EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Ovis sp.
US-09-359-167-4

Query Match	100.0%;	Score	2617;	DB	4;	Length	495;
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Db 421 YAGILLGTTNTFATIPGMIGPIIARSUPTENTIGEWQTVFCIAAANVFGAIFTFLPAKG 480
Qy 481 EVQNWAI SDHGHNRN 495
Db 481 EVQNWAI SDHGHNRN 495

RESULT 2
US-09-359-167-2
; Sequence 2, Application US/09359167
; Patent No. 6803448
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/01US
; CURRENT APPLICATION NUMBER: US/09/359,167
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 60-693,843
; EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-359-167-2

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Best Local Similarity 86.3%; Pred. No. 9.5e-244;
Matches 427; Conservative 39; Mismatches 29; Indels 0; Gaps 0;

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Qy 241 FILMICLVSDTPETHKTTITPEKEYISSLKNQSSQKSPWIPMLKSLPLWAIWVAHFS 300
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Qy 301 YNMTFYTLTLLPTMYKEILRFNIOENGFLSAVPYLGWLCWILSGQAADNLRARWNPST 360
Db 301 YNMTFYTLTLLPTMYKEILRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRARWNPST 360
Qy 361 LWRRVFSLIGMIGPAFLVAAGFGCDYSLAVAFLTISTTLGGFCSSGFSINHLDIAPS 420
Db 361 LCVRRI FSLIGMIGPAFLVAAGFGCDYSLAVAFLTISTTLGGFCSSGFSINHLDIAPS 420
Qy 421 YAGILLGTTNTFATIPGMIGPIIARSUPTENTIGEWQTVFCIAAANVFGAIFTFLPAKG 480
Db 421 YAGILLGTTNTFATIPGMIGPIIARSUPTENTIGEWQTVFCIAAANVFGAIFTFLPAKG 480
Qy 481 EVQNWAI SDHGHNRN 495
Db 481 EVQNWAI SDHGHNRH 495

RESULT 4
US-09-359-167-8
; Sequence 8, Application US/09359167
; Patent No. 6803448
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
```

```
RESULT 3
US-09-915-181A-7
; Sequence 7, Application US/09915181A
; Patent No. 6818391
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMEAU, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-9326100S
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-181A-7

Query Match 89.0%; Score 2329; DB 4; Length 495;
Best Local Similarity 86.3%; Pred. No. 9.5e-244;
Matches 427; Conservative 39; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MKSPVSDIAPSDGEGSDRTPLQAPRAEPAPVCCSARYNLAFSLFFGFFVLYSLRNL 60
Db 1 MRSFVRDLARNDGEESTDRTPLPGAPRAEAPVCCSARYNLAILAFPGFFIVVALRNL 60
Qy 61 SVALVDMVDSNTTAKDNRTSVECAHSAPIKVLHNQTKKKYRWDATQGWILGSFFFYGI 120
Db 61 SVALVDMVDSNTTLEDNRTSKACPEHSAPIKVHNQTKKKYQWDAETQGWILGSFFFYGI 120
Qy 121 ITQIPGGVVASRGGKLLGFGIPATAIFTLFTPLAADFGVGVALVALRLEGLEGVGYTP 180
Db 121 ITQIPGGVVASRGGKLLGFGILGTAVLTFTPLAADLGVGPLIVLRALLEGLEGVGYTP 180
Qy 181 AMHAMSSWAPPLERSKLLSISYAGAQIGTVVSLPSGVI CYNNWTVYVFFFGIVGIW 240
Db 181 AMHAMSSWAPPLERSKLLSISYAGAQIGTVISLPSGLI CYNNWTVYVFFFGTIGIFW 240
Qy 241 FILMICLVSDTPETHKTTITPEKEYISSLKNQSSQKSPWIPMLKSLPLWAIWVAHFS 300
Db 241 FLLMIWLVSDTPQKHRI SHYKEYISSLRNQLSSQKSPWPVPLKSLPLWAIWVAHFS 300
Qy 301 YNMTFYTLTLLPTMYKEILRFNIOENGFLSAVPYLGWLCWILSGQAADNLRARWNPST 360
Db 301 YNMTFYTLTLLPTMYKEILRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRARWNPST 360
Qy 361 LWRRVFSLIGMIGPAFLVAAGFGCDYSLAVAFLTISTTLGGFCSSGFSINHLDIAPS 420
Db 361 LCVRRI FSLIGMIGPAFLVAAGFGCDYSLAVAFLTISTTLGGFCSSGFSINHLDIAPS 420
Qy 421 YAGILLGTTNTFATIPGMIGPIIARSUPTENTIGEWQTVFCIAAANVFGAIFTFLPAKG 480
Db 421 YAGILLGTTNTFATIPGMIGPIIARSUPTENTIGEWQTVFCIAAANVFGAIFTFLPAKG 480
Qy 481 EVQNWAI SDHGHNRN 495
Db 481 EVQNWAI SDHGHNRH 495

RESULT 4
US-09-359-167-8
; Sequence 8, Application US/09359167
; Patent No. 6803448
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 05:11:02 ; Search time 108.026 seconds
(without alignments)
1772.222 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 2617

Sequence: 1 MKSPVSLAPSDGEGSDRT.....LFAKGEVQNWAIHQHGRN 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2617	100.0	495	3	AAY45088 Sheep GBS
2	2617	100.0	495	4	AAE06519 Sheep gro
3	2329	89.0	495	3	AAY45087 Partial h
4	2329	89.0	495	4	AAE06519 Sheep gro
5	2329	89.0	495	8	AAE06519 Sheep gro
6	2329	89.0	495	8	AAE06519 Sheep gro
7	2329	89.0	495	8	AAE06519 Sheep gro
8	2329	89.0	495	8	AAE06519 Sheep gro
9	2329	89.0	495	8	AAE06519 Sheep gro
10	2322	88.0	495	4	AAE06519 Sheep gro
11	1702	65.0	495	3	AAE06519 Sheep gro
12	1544	59.0	314	4	AAE06519 Sheep gro
13	1386	53.0	284	5	AAE06519 Sheep gro
14	1318	50.4	272	5	AAE06519 Sheep gro
15	1232	47.1	277	4	AAE06519 Sheep gro
16	1232	47.1	277	8	AAE06519 Sheep gro
17	1217	46.5	309	4	AAE06519 Sheep gro
18	991.5	37.9	559	4	AAE06519 Sheep gro
19	985.5	37.7	502	4	AAE06519 Sheep gro
20	985.5	37.7	502	4	AAE06519 Sheep gro
21	979	37.4	589	5	AAE06519 Sheep gro
22	979	37.4	589	6	AAE06519 Sheep gro
23	979	37.4	589	7	AAE06519 Sheep gro
24	979	37.4	589	7	AAE06519 Sheep gro
25	979	37.4	589	8	AAE06519 Sheep gro

26	969.5	37.0	601	7	ADD01410
27	968.5	37.0	493	8	ADN23181
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29	965	36.9	582	6	ABG74796
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32	965	36.9	582	7	ADCI15494
33	965	36.9	582	7	ADCI15492
34	962.5	36.8	582	6	ABG74795
35	962.5	36.8	582	7	ADCI15490
36	962.5	36.8	582	7	ADCI15490
37	958	36.6	566	7	ADJ95072
38	956.5	36.5	582	4	AAE079273
39	956.5	36.5	860	5	ABE07689
40	946.5	36.2	516	4	ABE67013
41	941	36.0	529	4	ABE63684
42	932	35.6	560	6	ABG74791
43	932	35.6	560	7	ADCI15482
44	932	35.6	560	7	ADCI15482
45	932	35.6	567	4	AAO13870

ALIGNMENTS

RESULT 1

RAY45088

ID AAY45088 standard; protein; 495 AA.

XX AAY45088;

XX AC

DT 31-MAY-2000 (first entry)

XX

DE Sheep GBS toxin receptor (SP55).

XX

KW Sheep GBS toxin receptor; group B beta-haemolytic streptococci; SP55;
KW pathological vascularisation; cancer metastases; angiogenesis; sheep;
KW neovascularisation; reperfusion injury; scarring; keloid;
KW chronic inflammation; rheumatoid arthritis; psoriasis; neural injury;
KW endothelial cell proliferation; antibacterial; anticancer;
KW anti-angiogenic; anti-inflammatory; anti-arthritis; anti-psoriatic.

OS Ovis sp.

XX

PH Key Location/Qualifiers

FT Peptide 7..22

FT /label= p55a

FT /note= "Immunogenic peptide"

FT Peptide 8..35

FT /label= p56a

FT /note= "Immunogenic peptide"

FT Modified-site 11..14

FT /label= CK2 phospho site

FT /note= "Predicted phosphorylation site"

FT Modified-site 17..19

FT /label= PKC phospho site

FT /note= "Predicted phosphorylation site"

FT Modified-site 37..39

FT /label= PKC phospho site

FT /note= "Predicted phosphorylation site"

FT Domain 42..58

FT /note= "Predicted transmembrane domain"

FT Modified-site 55..57

FT /label= PKC phospho site

FT /note= "Predicted phosphorylation site"

FT Modified-site 59..62

FT /label= PKC phospho site

FT /note= "Predicted phosphorylation site"

FT Peptide 71..84

FT /label= p57a

FT /note= "Immunogenic peptide"

FT Modified-site 71..74

FT /label= p57a

FT /note= "Immunogenic peptide"

FT Modified-site 73..76

FT /label= p57a

FT /note= "Immunogenic peptide"

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 FT 142. .147
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 FT 172. .177
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 FT 259. .262
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 FT 269. .271
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 FT 276. .278
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 FT /note= "Inner boundary of transmembrane domain"
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 FT 390. .407
 FT /note= "Outer boundary of transmembrane domain"
 FT 390. .406
 FT /note= "Inner boundary of transmembrane domain"
 FT 403. .408
 FT /note= "Predicted myristylation site"

FT Modified-site 423. .428
 FT /note= "Predicted myristylation site"
 FT Modified-site 427. .432
 FT /note= "Predicted myristylation site"
 FT Modified-site 452. .455
 FT /label= CK2 phospho site
 FT /note= "Predicted phosphorylation site"
 FT 456. .479
 FT /note= "Outer boundary of transmembrane domain"
 FT 458. .474
 FT /note= "Inner boundary of transmembrane domain"
 FT XX
 FN WO200005375-A1.
 XX 03-FEB-2000.
 XX 22-JUL-1999; 99WO-US016676.
 XX 22-JUL-1998; 98US-0093843P.
 XX (UYVA-) UNIV VANDERBILT.
 XX Hellergqvist CG, Fu C;
 DR WPI; 2000-205377/18.
 DR N-PSDB; AAZ50876.
 XX
 PT New polynucleotide encoding mammalian receptor for streptococcus toxin,
 PT useful for diagnosis and treatment of, e.g. pneumonia in neonates.
 XX
 PS Claim 10; Page 22; 109pp; English.
 XX
 CC The present sequence is sheep GBS (group B beta-haemolytic streptococci)
 CC toxin receptor (SP55). Sheep GBS toxin receptor is an integral protein
 CC with seven transmembrane domains. Expression vectors comprising the
 CC coding region can be transformed into host cells to express GBS toxin
 CC receptor and its fragments. Detecting the receptor in tissues is used to
 CC diagnose pathological vascularisation, e.g. for detecting cancer
 CC metastases. GBS toxin receptors are useful for treating conditions
 CC associated with pathological angiogenesis or neovascularisation
 CC (specifically cancer, reperfusion injury, scarring during wound healing,
 CC keloids, chronic inflammation (rheumatoid arthritis or psoriasis) or
 CC neural injury), and to raise specific antibodies used for treating early
 CC onset disease. Inhibitors of this receptor are useful for treating
 CC pathological or hypoxia-induced endothelial cell proliferation and
 CC migration
 XX
 SQ Sequence 495 AA;
 Query Match 100.0%; Score 2617; DB 3; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1.8e-273;
 Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKSPVSDIAPSDGEGSDRTPLLQAPRAPAPVCCSARYNLAPLSPFGFVLYSLRVNL 60
 Db 1 MKSPVSDIAPSDGEGSDRTPLLQAPRAPAPVCCSARYNLAPLSPFGFVLYSLRVNL 60
 Qy 61 SVALVDMVDSNTTAKONRTSYECAHSAPIKVLHNOTGKKYRWDATQGWILGSFFVGYI 120
 Db 61 SVALVDMVDSNTTAKONRTSYECAHSAPIKVLHNOTGKKYRWDATQGWILGSFFVGYI 120
 Qy 121 ITQIPGGYVASRSGGKLLGFGIFATAIFTLPTLAADFGVGVGALVALRALEGLGEGVTYP 180
 Db 121 ITQIPGGYVASRSGGKLLGFGIFATAIFTLPTLAADFGVGVGALVALRALEGLGEGVTYP 180
 Qy 181 AMIAMSWSWAPPLERSKLLSISYAGALQGTWVSLPSLPGVTCYMNWTVYVFFGIVGIW 240
 Db 181 AMIAMSWSWAPPLERSKLLSISYAGALQGTWVSLPSLPGVTCYMNWTVYVFFGIVGIW 240
 Qy 241 FILWICLVSDTPETHKTTITPYEKEYITLSSLNQISSOKSVPMPLKSLPLWAIWVAHFS 300
 Db 241 FILWICLVSDTPETHKTTITPYEKEYITLSSLNQISSOKSVPMPLKSLPLWAIWVAHFS 300

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2005, 05:13:45 ; Search time 114.894 Seconds
(without alignments)
2388.931 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 2836

Sequence: 1 MAAGAMTPRPVQPARPGGF.....LFAKGEVQNALNDHGHGRH 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2621	92.4	495	1 S175_HUMAN	Q9nra2 homo sapien
2	2329	82.1	495	1 S175_SHEEP	Q9mzdl ovine aries
3	2298	81.0	495	1 S175_MOUSE	Q8bn82 mus musculus
4	1051	37.1	544	2 Q7Q580	Q7q580 anopheles g
5	996.5	35.1	559	2 Q9VYG7	Q9vyg7 drosophila
6	992	35.0	502	2 Q9VDM0	Q9vdm0 drosophila
7	991	34.9	476	2 Q7Q579	Q7q579 anopheles g
8	987	34.8	493	1 YLD2_CAEEL	Q03567 caenorhabdi
9	970	34.2	582	2 Q920B7	Q920b7 mus musculus
10	970	34.2	582	2 Q9J112	Q9j112 rattus norv
11	966.5	34.1	584	2 Q8AW47	Q8aw47 brachydanio
12	965.5	34.0	582	2 Q9P2U8	Q9p2u8 homo sapien
13	965	34.0	582	2 Q8BLE7	Q8ble7 mus musculus
14	955	33.7	589	2 Q8NDX2	Q8ndx2 homo sapien
15	954.5	33.7	588	2 Q8K1Q1	Q8k1q1 rattus norv
16	954.5	33.7	588	2 Q7TSP2	Q7tsf2 rattus norv
17	946.5	33.4	479	2 Q23514	Q23514 caenorhabdi
18	945	33.3	601	2 Q8BFU8	Q8bfu8 mus musculus
19	941	33.2	560	2 Q9P2U7	Q9p2u7 homo sapien
20	939.5	33.1	576	2 Q2INC8	Q2inc8 xenopus lae
21	936	33.0	560	2 Q62634	Q62634 rattus norv
22	932	32.9	560	2 Q6PCD0	Q6pcd0 homo sapien
23	928.5	32.7	529	1 PICO_DRONE	Q9v785 drosophila
24	917	32.3	483	1 PICO_DROAN	Q61369 drosophila
25	913.5	32.2	576	2 Q715L3	Q715l3 xenopus lae
26	905	31.9	955	2 Q7Q367	Q7q367 anopheles g
27	895	31.6	466	2 Q96LH1	Q96lh1 homo sapien
28	889.5	31.4	533	2 Q7Q1S5	Q7q1s5 anopheles g
29	876	30.9	497	2 Q9Y2C5	Q9y2c5 homo sapien
30	870.5	30.7	535	2 Q7PMK4	Q7pmk4 anopheles g
31	856	30.2	479	2 Q9W4G7	Q9w4g7 drosophila

32	856	30.2	498	2 Q8CJH9	Q8cjh9 rattus norv
33	852.5	30.1	485	2 Q7PSC6	Q7psc6 anopheles g
34	852.5	30.1	496	2 Q9VKC9	Q9vkc9 drosophila
35	845	29.8	632	2 Q8CP76	Q8cp76 drosophila
36	838.5	29.6	481	2 Q9VJW8	Q9vjw8 drosophila
37	837.5	29.5	470	2 Q7YT27	Q7yt27 drosophila
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39	822.5	29.0	465	1 NPT1_RABIT	Q28722 o renal sod
40	822	29.0	498	2 Q8VCY5	Q8vcy5 mus musculus
41	821.5	29.0	512	2 Q9VPX2	Q9vpv2 drosophila
42	819	28.9	475	2 Q6AZ69	Q6az69 rattus norv
43	814.5	28.7	465	2 Q91WV5	Q91wv5 mus musculus
44	814.5	28.7	467	2 Q7VQJ7	Q7vqj7 sus scrofa
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ALIGNMENTS

RESULT 1

ID S175_HUMAN STANDARD; PRT; 495 AA.
AC Q9NRA2; Q8NBR5; Q9UGH0;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sialin (Solute carrier family 17 member 5) (Sodium/sialic acid
DE cotransporter) (AST) (Membrane glycoprotein HP59).
GN Name=SLC17A5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=11751519;
RA Fu C., Bardhan S., Cetateanu N.D., Wamil B.D., Wang Y., Yan H.-P.,
RA Shi E., Carter C., Venkov C., Yakes F.M., Page D.L., Lloyd R.S.,
RA Mernaugh R.L., Hellerqvist C.G.;
RT "Identification of a novel membrane protein, HP59, with therapeutic
potential as a target of tumor angiogenesis.";
RL Clin. Cancer Res. 7:4182-4194(2001).
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RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, TISSUE SPECIFICITY, VARIANT
SD CYS-39, AND VARIANTS ISSD 268-SER--ASN-272 DEL; ARG-193 AND
ARG-334.
RX MEDLINE=20047778; PubMed=10581036; DOI=10.1038/70585;
RA Verheijen F.W., Verbeek E., Aula N., Beerens C.E.M.T., Havelaar A.C.,
RA Joosse M., Peltonen L., Aula P., Gaijaard H., Van der Spek P.J.,
RA Mancini G.M.S.;
RT "A new gene, encoding an anion transporter, is mutated in sialic acid
storage diseases.";
RL Nat. Genet. 23:462-465(1999).
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RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Negahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki K., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotaka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Highigaki H., Watanabe T., Sudiama A., Takemoto M., Kawakami B.,
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RA Fujimori Y., Komiya M., Tasigai H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
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RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
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RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Colon;
RX MEDLINE=23289257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Feilgenbaum J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krawczynski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP VARIANTS SD CVS-39 AND GLU-136, AND VARIANTS ISSD 268-SER--ASN-272
RP DEL; ARG-183; ARG-334 AND VAL-371.
RX PubMed=10947946;
RA Aul N., Salomaa P., Timonen R., Verheijen F., Mancini G.M.S.,
RA Maenonen J.-E., Aul P., Peltonen L.;
RT "The spectrum of SLC17A5-gene mutations resulting in free sialic acid-
RT storage diseases indicates some genotype-phenotype correlation.";
RL Am. J. Hum. Genet. 67:832-840(2000).
RN [6]
RP VARIANT SD CVS-39.
RX PubMed=12794687; DOI=10.1002/ajmg.a.10246;
RA Martin R.A., Slaughter R., Natowicz M., Pearlman K., Orvisky E.,
RA Krasnewich D., Kleta R., Huizing M., Gahl W.A.;
RT "Sialic acid storage disease of the Salla phenotype in American
RT monozygous twin female sibs.";
RL Am. J. Med. Genet. 120:23-27(2003).
CC -!- FUNCTION: Primary solute translocator for anionic substances;
CC particularly it is a free sialic acid transporter in the lysosomes
CC (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal
CC (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NRA2-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NRA2-2; Sequence=VSP_010482, VSP_010483;
CC Note=NO experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Found in fetal lung and small intestine, and
CC at lower level in fetal skin and muscle. In the adult, detected in
CC placenta, kidney and pancreas. Abundant in the endothelial cells
CC of tumors from ovary, colon, breast and lung, but is not detected
CC in endothelial cells from the corresponding normal tissues.
CC -!- DISEASE: Defects in SLC17A5 are the cause of Salla disease (SD)

CC [MIM:604369]; also known as Finnish type sialuria, a sialic acid
CC storage disease (SASD). SASDs are autosomal recessive
CC neurodegenerative disorders characterized by hypotonia, cerebellar
CC ataxia and mental retardation. They are caused by a defect in the
CC metabolism of sialic acid which results in increased urinary
CC excretion of unconjugated sialic acid, specifically N-
CC acetylneuraminic acid. Enlarged lysosomes are seen on electron
CC microscopic studies. Clinical symptoms of SD present usually at
CC age less than 1 year and progression is slow.
CC -!- DISEASE: Defects in SLC17A5 are the cause of infantile sialic acid
CC storage disorder (ISSD) [MIM:269920]; also known as N-
CC acetylneuraminic acid storage disease (NSD). ISSD is a severe form
CC of sialic acid storage disease. Affected newborns exhibit
CC visceromegaly, coarse features and failure to thrive immediately
CC after birth. These patients have a shortened life span, usually
CC less than 2 years.
CC -!- SIMILARITY: Belongs to the major facilitator (MFS) superfamily.
CC Sodium/anion cotransporter family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement [see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch].
CC -----
CC EMBL; AF244577; AAF97769.1; ALT_INIT.
CC EMBL; AJ387747; CAB62540.1; -.
CC EMBL; AK075320; BAC11546.1; -.
CC EMBL; BC020961; AAH20961.1; -.
CC Genew; HGNC:10933; SLC17A5.
CC MIM; 604322; -.
CC MIM; 269920; -.
CC MIM; 604369; -.
CC InterPro; IPR007114; MFS.
CC InterPro; IPR005828; Subtransporter.
CC Pfam; PF00083; Sugar tr; 1.
CC PROSITE; PS00850; MFS; 1.
CC Alternative splicing; Disease mutation; Lysosome; Symport;
CC Transmembrane; transport.
CC TRANSMEM 42 62 Potential.
CC TRANSMEM 110 130 Potential.
CC TRANSMEM 137 157 Potential.
CC TRANSMEM 159 179 Potential.
CC TRANSMEM 201 221 Potential.
CC TRANSMEM 228 248 Potential.
CC TRANSMEM 280 300 Potential.
CC TRANSMEM 329 349 Potential.
CC TRANSMEM 366 386 Potential.
CC TRANSMEM 392 412 Potential.
CC TRANSMEM 424 444 Potential.
CC TRANSMEM 458 478 Potential.
CC VARSPPLIC 274 276 Potential.
CC VARSPPLIC 278 495 Missing (in isoform 2).
CC FT Missing (in isoform 2).
CC FT /FTid=VSP_010483.
CC FT R -> C (in SD; frequent mutation in
CC FT Finland).
CC FT /FTid=VAR_018684.
CC FT K -> E (in SD).
CC FT /FTid=VAR_018685.
CC FT H -> R (in ISSD).
CC FT /FTid=VAR_018686.
CC FT Missing (in ISSD).
CC FT /FTid=VAR_018687.
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CC FT /FTid=VAR_018688.
CC FT G -> V (in ISSD).
CC FT /FTid=VAR_018689.
CC FT SEQUENCE 495 AA; 54639 MW; 5C6C154B3E93A19E CRC64;
CC Query Match 92.4%; Score 2621; DB 1; Length 495;

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:16:27 ; Search time 27.0339 Seconds
(without alignments)
1907.682 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 2836

Sequence: 1 MAAGAMTPRPVQPARPGGF.....LFAKGEVQWALNDHGHGRH 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	987	34.8	493	2 G88553	protein C38C10.2 [
2	967	34.1	472	2 S28286	hypothetical prote
3	936	33.0	560	2 I59302	brain specific Na+
4	822.5	29.0	465	2 A56410	sodium/phosphate t
5	809.5	28.5	465	2 S69915	sodium-phosphate t
6	808	28.5	563	2 T43650	probable sodium-de
7	808	28.5	576	2 H88548	protein ZK512.6 [l
8	801.5	28.3	467	2 A48916	sodium phosphate t
9	797.5	28.1	573	2 T23589	hypothetical prote
10	786.5	27.7	465	2 I39473	Na+-dependent phos
11	767.5	27.1	544	2 T24633	hypothetical prote
12	747	26.3	512	2 H84698	hypothetical prote
13	629.5	22.2	501	2 B89135	protein F25G6.7 [l
14	562	19.8	413	2 T01534	hypothetical prote
15	531	18.7	537	2 T45634	hypothetical prote
16	530.5	18.7	466	2 S40767	hypothetical prote
17	492.5	17.4	561	2 D84800	hypothetical prote
18	486.5	17.2	568	2 S44742	C02C2.4 protein -
19	476.5	16.8	592	2 T25419	hypothetical prote
20	460.5	16.2	516	2 T24729	hypothetical prote
21	452	15.9	530	2 T29418	hypothetical prote
22	445	15.7	380	2 T29248	hypothetical prote
23	444.5	15.7	543	2 T32496	hypothetical prote
24	432.5	15.3	499	2 T15201	hypothetical prote
25	431	15.2	506	2 T29968	hypothetical prote
26	419.5	14.8	493	2 T25357	hypothetical prote
27	392.5	13.8	478	2 T33940	hypothetical prote
28	389.5	13.7	445	2 T23590	hypothetical prote
29	388.5	13.7	462	2 T34365	hypothetical prote

30	386.5	13.6	473	2 T31717	hypothetical prote
31	380.5	13.4	425	2 A90055	hypothetical prote
32	372	13.1	420	2 S44900	ZK652.10 protein -
33	370.5	13.1	428	2 AD0675	membrane transport
34	362	12.8	485	2 T24115	hypothetical prote
35	360	12.7	455	1 H69752	probable glucarat
36	357.5	12.6	455	2 T34366	hypothetical prote
37	357	12.6	452	2 AEO861	probable glucarate
38	355.5	12.5	659	2 T33557	hypothetical prote
39	353	12.4	516	2 T27092	hypothetical prote
40	349	12.3	450	2 A65061	probable glucarate
41	349	12.3	450	2 C85930	probable glucarate
42	349	12.3	450	2 A91085	probable transport
43	339.5	12.0	445	1 D65171	hypothetical 48.8
44	336.5	11.9	493	2 T19383	hypothetical prote
45	334	11.8	487	2 T23776	hypothetical prote

ALIGNMENTS

RESULT 1

G88553

protein C38C10.2 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: G88553

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: G88553

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-493 <STO>

A:Cross-references: UNIPROT:Q03567; GB:chr_III; PIDN:CAA79549.1; PID:G3874873; GSPDB:GNO0

C:Genetics:

A:Gene: C38C10.2

A:Map position: 3

Query Match

Best Local Similarity 34.8%; Score 987; DB 2; Length 493;

Matches 194; Conservative 94; Mismatches 179; Indels 22; Gaps 6;

QY 55 BESTDRTPLLPACPAEAAAPVCCSARYNLAILAFPGFIVVALRVNLVALVDMVDSNTT 114

Db 2 EGATTKRLVP-----STRFALSLVMFFGCLVYMTNTNMFVAVCMVNEKT 49

QY 115 LEDNRTSKACPEHSAPIKVHNOTGKKYQWDAETQGTWILSGFFFYGYIITQIPGGYVASKI 174

Db 50 DTGVEKVSRCGKEMTPVESNSVIG-EPDWDKQITGMVLSSFFFYGYIGIIGHLASRY 108

QY 175 GKMLLGFILGTAVLTFTPIAADLGVPLIVLRALEGLGEGVTFPAHMAWSSWAPPL 234

Db 109 GKKWFWFTILGSAALLTLNPAARTSEYALAILRAAIGFLQGAFFPAHMTWMSVGMGPL 168

QY 235 ERSKLLTSYAGAOLGTIVISLPLSLGIICYY---NMNVTYVFFYFGTIGIFWFLWLWLVSND 291

Db 169 ELSVLTGYTYAGAIGNIVLPLSGFLCEYFGDGWSPSIFYIIIGVGLWTAVMWYVSSD 228

QY 292 TPQKHKRISHYKEYYILSSLRNQLSSQ----KSPVPWVPLKSLPLWAIWAFHSYNNWTFY 347

Db 229 KPATHPRITPEKQYIVTAVEASMGDKTGVSPSPWIKILTSPA WACWAGHAFGAGWAGY 288

QY 348 TLLTLLPTYMKEIIRFVQENGFLSSPLGSLWLCMLSLSGOAAADNLRKWNFSLCVRRI 407

Db 289 TMLVSLPSFLKDVGLGNLSLGAVASIPYIAYFLAINAGGAVLADTLRSKGLISTLNTERR 348

QY 408 FSLIGMTGPAVFLVAAGFIGDYS-LAVAFUTISTTLGGFCSSGFSINHLIAPSYAGIL 466

Db 349 ANLVALIGQGFILVASGYCCGQDVLVIIFITCGMAISGLQYGFVNVNLEIAPFSGTV 408

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:22:07 ; Search time 115.414 Seconds
(without alignments)
1794.174 Million cell updates/sec

Title: US-09-776-865-2
Perfect score: 2836
Sequence: 1 MAAGMTPPRPVQPARPGF.....LPAKGEVQNALNDHGHHRH 536

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2836	100.0	536	9	US-09-776-865-2
2	2836	100.0	536	17	US-10-823-506-8
3	2621	92.4	495	9	US-09-915-181A-7
4	2621	92.4	495	16	US-10-755-889-588
5	2621	92.4	495	17	US-10-823-506-2
6	2329	82.1	495	9	US-09-776-865-4
7	2329	82.1	495	17	US-10-823-506-4
8	1698	59.9	495	17	US-10-823-506-10
9	1698	59.9	495	17	US-10-823-506-12
10	1521	53.6	284	15	US-10-264-049-2477
11	1451	51.2	272	15	US-10-264-237-2351

12	987	34.8	493	15	US-10-369-493-5834
13	970	34.2	578	9	US-09-740-041-4
14	970	34.2	578	14	US-10-389-967-4
15	970	34.2	582	9	US-09-915-181A-4
16	970	34.2	582	15	US-10-205-331-7
17	970	34.2	582	16	US-10-734-731-12
18	970	34.2	582	16	US-10-734-731-14
19	970	34.2	582	16	US-10-807-500-12
20	970	34.2	582	16	US-10-807-500-14
21	965.5	34.0	582	16	US-10-734-731-10
22	965.5	34.0	582	16	US-10-807-500-10
23	955	33.7	589	9	US-09-740-041-2
24	955	33.7	589	14	US-10-389-967-2
25	955	33.7	589	18	US-10-499-731-28
26	945	33.3	601	18	US-10-499-731-46
27	941	33.2	560	16	US-10-734-731-2
28	941	33.2	560	16	US-10-807-500-2
29	940.5	33.2	566	15	US-10-287-226-300
30	940	33.1	566	15	US-10-314-790-5
31	940	33.1	560	16	US-10-734-731-4
32	940	33.1	560	16	US-10-807-500-4
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34	936	33.0	560	9	US-09-991-212A-4
35	936	33.0	560	9	US-09-915-181A-5
36	936	33.0	560	10	US-09-965-522-4
37	936	33.0	560	16	US-10-734-731-6
38	936	33.0	560	16	US-10-734-731-8
39	936	33.0	560	16	US-10-807-500-6
40	936	33.0	560	16	US-10-807-500-8
41	936	33.0	560	17	US-10-877-818-4
42	935	33.0	850	9	US-09-915-181A-3
43	808	28.5	563	9	US-09-915-181A-6
44	808	28.5	576	14	US-10-014-079A-1
45	808	28.5	576	15	US-10-369-493-5823

ALIGNMENTS

RESULT 1
US-09-776-865-2
; Sequence 2, Application US/09776865
; Patent No. US20020061846A1
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; TITLE OF INVENTION: Methods for Preventing or Attenuating Pathoangiogenic Conditions
; FILE REFERENCE: 22100-0100 46126-252687
; CURRENT APPLICATION NUMBER: US/09/776.865
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,870
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-865-2

Query Match	100.0%	Score 2836	DB 9	Length 536
Best Local Similarity	100.0%	Pred. No. 3.6e-249	Mismatches 0	Indels 0
Matches 536	Conservative 0			Gaps 0
Oy	1	MAAGMTPPRPVQPARPGFSGRRSLCCQVASTPAHVGMRSFVRDLARNDEESTDR	60	
Db	1	MAAGMTPPRPVQPARPGFSGRRSLCCQVASTPAHVGMRSFVRDLARNDEESTDR	60	
Oy	61	TPLPAGPRAEAPVCCSARYNLAILAFPGFPIYALRVNLSVALVDMVDSNTTLEDR	120	
Db	61	TPLPAGPRAEAPVCCSARYNLAILAFPGFPIYALRVNLSVALVDMVDSNTTLEDR	120	
Oy	121	SKACPEHSAPTKVHNNTGKKYQWDASTQWLGSLFFVGYIITOTIPGYVASKIGKMLL	180	

Db 121 SKACPEHSAPIKVHNTQTKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGKMLL 180
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Db 181 GFGILGTAVLTFTPIAADLGVGPLIVLRALEGLGEGVTFPAMHAMWSSWAPPLERSKLL 240
Qy 241 SISVAGAOLGTVISLPLSGIICYYNNWTVYVFFGTIGIFWFLMWLVSDTPQKHKRIS 300
Db 241 SISVAGAOLGTVISLPLSGIICYYNNWTVYVFFGTIGIFWFLMWLVSDTPQKHKRIS 300
Qy 301 HYEKEYILSSLRNQLSSQKSPVWPVILKSLPLWAIWVAHFSYNWTFYLLTLLPTMYKEI 360
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Db 361 LRFNVQENGFLSSLPYLGSWLCMLSGQAADNLRAKNFSTLCVRRIFSLIGMIGPAVFL 420
Qy 421 VAAGFIGCDYSLAVAFITITTLGGFCSSGFSINHLDIAPSYAGILLGITNTFTATIPGMV 480
Db 421 VAAGFIGCDYSLAVAFITITTLGGFCSSGFSINHLDIAPSYAGILLGITNTFTATIPGMV 480
Qy 481 GPVIAKSLTPDNTVGEWQTVFYIAAINVFGAIFFTLFAKGEVQNWALNDHHGHRH 536
Db 481 GPVIAKSLTPDNTVGEWQTVFYIAAINVFGAIFFTLFAKGEVQNWALNDHHGHRH 536

RESULT 2

US-10-823-506-8
; Sequence 8, Application US/10823506
; Publication No. US20050002931A1
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/0105
; CURRENT APPLICATION NUMBER: US/10/823,506
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/359,167
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-693,843
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 8
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-823-506-8

Query Match 100.0%; Score 2836; DB 17; Length 536;
Best Local Similarity 100.0%; Pred. No. 3.6e-249;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGAMTPRPVQPARPGFGLSGRRSLLCQVASTPAHVGMRSVPRDLARNDGEESTDR 60
Db 1 MAAGAMTPRPVQPARPGFGLSGRRSLLCQVASTPAHVGMRSVPRDLARNDGEESTDR 60
Qy 61 TPLLPAPRAEAPVCCSARNLAILAFPGFIVVALRVNLSVALVMDVDSNTTLEDNRT 120
Db 61 TPLLPAPRAEAPVCCSARNLAILAFPGFIVVALRVNLSVALVMDVDSNTTLEDNRT 120
Qy 121 SKACPEHSAPIKVHNTQTKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGKMLL 180
Db 121 SKACPEHSAPIKVHNTQTKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGKMLL 180
Qy 181 GFGILGTAVLTFTPIAADLGVGPLIVLRALEGLGEGVTFPAMHAMWSSWAPPLERSKLL 240
Db 181 GFGILGTAVLTFTPIAADLGVGPLIVLRALEGLGEGVTFPAMHAMWSSWAPPLERSKLL 240
Qy 241 SISVAGAOLGTVISLPLSGIICYYNNWTVYVFFGTIGIFWFLMWLVSDTPQKHKRIS 300
Db 241 SISVAGAOLGTVISLPLSGIICYYNNWTVYVFFGTIGIFWFLMWLVSDTPQKHKRIS 300

Qy 301 HYEKEYILSSLRNQLSSQKSPVWPVILKSLPLWAIWVAHFSYNWTFYLLTLLPTMYKEI 360
Db 301 HYEKEYILSSLRNQLSSQKSPVWPVILKSLPLWAIWVAHFSYNWTFYLLTLLPTMYKEI 360
Qy 361 LRFNVQENGFLSSLPYLGSWLCMLSGQAADNLRAKNFSTLCVRRIFSLIGMIGPAVFL 420
Db 361 LRFNVQENGFLSSLPYLGSWLCMLSGQAADNLRAKNFSTLCVRRIFSLIGMIGPAVFL 420
Qy 421 VAAGFIGCDYSLAVAFITITTLGGFCSSGFSINHLDIAPSYAGILLGITNTFTATIPGMV 480
Db 421 VAAGFIGCDYSLAVAFITITTLGGFCSSGFSINHLDIAPSYAGILLGITNTFTATIPGMV 480
Qy 481 GPVIAKSLTPDNTVGEWQTVFYIAAINVFGAIFFTLFAKGEVQNWALNDHHGHRH 536
Db 481 GPVIAKSLTPDNTVGEWQTVFYIAAINVFGAIFFTLFAKGEVQNWALNDHHGHRH 536

RESULT 3

US-09-915-181A-7
; Sequence 7, Application US/09915181A
; Patent No. US20020098473A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMEAU, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-932610US
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-181A-7

Query Match 92.4%; Score 2621; DB 9; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.2e-229;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 MRSVPRDLARNDGEESTDRTPLLPGAPRAEAPVCCSARNLAILAFPGFIVVALRVNL 101
Db 1 MRSVPRDLARNDGEESTDRTPLLPGAPRAEAPVCCSARNLAILAFPGFIVVALRVNL 60
Qy 102 SVALVDMVDSNTTLEDNRTSKACPEHSAPIKVHNTQTKKYQWDAETQGWILGSFFYGYI 161
Db 61 SVALVDMVDSNTTLEDNRTSKACPEHSAPIKVHNTQTKKYQWDAETQGWILGSFFYGYI 120
Qy 162 ITQIPGGYVASKIGKMLLFGILGTAVLTFTPIAADLGVGPLIVLRALEGLGEGVTFP 221
Db 121 ITQIPGGYVASKIGKMLLFGILGTAVLTFTPIAADLGVGPLIVLRALEGLGEGVTFP 180
Qy 222 AMHAMWSSWAPPLERSKLLSISVAGAOLGTVISLPLSGIICYYNNWTVYVFFGTIGIFW 281
Db 181 AMHAMWSSWAPPLERSKLLSISVAGAOLGTVISLPLSGIICYYNNWTVYVFFGTIGIFW 240
Qy 282 FLWLVSDTPQKHKRISHYEKEYILSSLRNQLSSQKSPVWPVILKSLPLWAIWVAHFS 341
Db 241 FLWLVSDTPQKHKRISHYEKEYILSSLRNQLSSQKSPVWPVILKSLPLWAIWVAHFS 300
Qy 342 YNWTFTYLLTLLPTMYKEILRFNVQENGFLSSLPYLGSWLCMLSGQAADNLRAKNFST 401
Db 301 YNWTFTYLLTLLPTMYKEILRFNVQENGFLSSLPYLGSWLCMLSGQAADNLRAKNFST 360
Qy 402 LCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFITITTLGGFCSSGFSINHLDIAPS 461
Db 361 LCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFITITTLGGFCSSGFSINHLDIAPS 420

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:00:41 ; Search time 10.6731 Seconds
(without alignments)
1304.461 Million cell updates/sec

Title: US-09-776-865-2
Perfect score: 2836
Sequence: 1 MAAGAMTPPRPVQPARPGF.....LFAKGEVQNALNDHGHGRH 536

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2836	100.0	536	4	US-09-359-167-8
2	2804.5	98.9	585	4	US-09-949-016-7705
3	2621	92.4	495	4	US-09-359-167-2
4	2621	92.4	495	4	US-09-915-181A-7
5	2329	82.1	495	4	US-09-359-167-4
6	1698	59.9	495	4	US-09-359-167-10
7	1698	59.9	495	4	US-09-359-167-12
8	970	34.2	578	4	US-09-740-041-4
9	970	34.2	582	4	US-09-915-181A-4
10	955	33.7	589	4	US-09-740-041-2
11	941	33.2	567	4	US-09-949-016-11354
12	940	33.1	560	4	US-08-647-484-2
13	940	33.1	560	1	US-08-647-481-2
14	940	33.1	560	1	US-08-430-033A-2
15	940	33.1	560	5	PCT-US96-05792-2
16	936	33.0	560	2	US-08-805-118-4
17	936	33.0	560	3	US-09-391-958-4
18	936	33.0	560	4	US-09-915-181A-5
19	935	33.0	850	4	US-09-915-181A-3
20	876	30.9	497	4	US-09-949-016-6616
21	810	28.6	552	4	US-09-270-767-45540
22	808	28.5	563	4	US-09-915-181A-6
23	808	28.5	576	3	US-08-864-785-1
24	806.5	28.4	465	4	US-09-915-181A-8
25	801.5	28.3	467	2	US-08-805-118-3
26	801.5	28.3	467	3	US-09-391-958-3
27	793	28.0	480	2	US-08-724-334A-9

28	686	24.2	436	4	US-09-949-016-11448	Sequence 11448, A
29	686	24.2	470	2	US-08-724-394A-10	Sequence 10, Appl
30	615.5	21.7	401	2	US-08-805-118-1	Sequence 1, Appl
31	615.5	21.7	401	3	US-09-391-958-1	Sequence 11, Appl
32	592.5	20.9	480	2	US-08-724-394A-11	Sequence 1053, Ap
33	562	19.8	380	4	US-09-949-016-7053	Sequence 9663, Ap
34	453	16.0	460	4	US-09-489-039A-9663	Sequence 45527, A
35	445.5	15.7	234	4	US-09-270-767-45527	Sequence 45384, A
36	375	13.2	186	4	US-09-270-767-45384	Sequence 13633, A
37	373	13.2	434	4	US-09-489-039A-13633	Sequence 6912, Ap
38	370	13.0	470	4	US-09-328-352-6912	Sequence 14, Appl
39	369	13.0	439	3	US-09-172-952-14	Sequence 12, Appl
40	369	13.0	439	4	US-09-922-501-12	Sequence 61037, A
41	368	13.0	439	4	US-09-270-767-61037	Sequence 9942, Ap
42	355.5	12.5	455	4	US-09-489-039A-9942	Sequence 10630, A
43	346.5	12.2	459	4	US-09-489-039A-10630	Sequence 32926, A
44	332	11.7	163	4	US-09-270-767-32926	Sequence 48143, A
45	332	11.7	163	4	US-09-270-767-48143	

ALIGNMENTS

RESULT 1
US-09-359-167-8
; Sequence 8, Application US/09359167
; Patent No. 6803448
; GENERAL INFORMATION:
; APPLICANT: Hellergvist, Carl
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/01US
; CURRENT APPLICATION NUMBER: US/09/359,167
; EARLIER FILING DATE: 1999-07-21
; EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-359-167-8

Query Match	100.0%;	Score	2836;	DB	4;	Length	536;
Best Local Similarity	100.0%;	Pred. No.	7.8e-294;				
Matches	536;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MAAGAMTPPRPVQPARPGFGLSGRRSILCOVASTPAHVGVMSRSPVRDLARNDCGEESTDR	60				
Db	1	MAAGAMTPPRPVQPARPGFGLSGRRSILCOVASTPAHVGVMSRSPVRDLARNDCGEESTDR	60				
Qy	61	TPLLPGAPRAEAAAPVCCSARYNLAILAFFGFFIYVALRVNLVALVDMVDSNTTLEDNRT	120				
Db	61	TPLLPGAPRAEAAAPVCCSARYNLAILAFFGFFIYVALRVNLVALVDMVDSNTTLEDNRT	120				
Qy	121	SKACPEHSAPIKVHNNQTKKKYQWDAETQGWILGSPFYGIITQIPGVYASKIGKRMLL	180				
Db	121	SKACPEHSAPIKVHNNQTKKKYQWDAETQGWILGSPFYGIITQIPGVYASKIGKRMLL	180				
Qy	181	GFGILGTAVLTFTPIAADLGVGLIIVLRALEGEGVTPPAMHAMSSWAPPLERSKLL	240				
Db	181	GFGILGTAVLTFTPIAADLGVGLIIVLRALEGEGVTPPAMHAMSSWAPPLERSKLL	240				
Qy	241	SISVAGAQLGTVISLPLSGIICYYMNTYVYFFGTGIGIYFWLLWILVSDTPQKHRRIS	300				
Db	241	SISVAGAQLGTVISLPLSGIICYYMNTYVYFFGTGIGIYFWLLWILVSDTPQKHRRIS	300				
Qy	301	HYKEYILSLRLNQLSSQKSPVWPILKSLPLMAIVVAHFYSYNTFTYLLTLLPTFMKEI	360				
Db	301	HYKEYILSLRLNQLSSQKSPVWPILKSLPLMAIVVAHFYSYNTFTYLLTLLPTFMKEI	360				
Qy	361	LRFNQENGFLSSLPYLGSWLCMLSCMLSLRAKWNFSTLCVRRIFSLIGMIGPAVFL	420				

Db 361 LRFNVQENGLSSLYLGSWLCMILSGQAADNLRKWNFSTLCVRRIFSLIGMIGPAVFL 420
Qy 421 VAAGFIGCDYSLAVAFLLITSTTLGGFCSSGFSINHLDIAPSVAGILLGTTNTFATIPGMV 480
Db 421 VAAGFIGCDYSLAVAFLLITSTTLGGFCSSGFSINHLDIAPSVAGILLGTTNTFATIPGMV 480
Qy 481 GPVIAKSLTPDNTVGEWQTVFYIAAANVFGAIFFTLFAKGEVQWALNDHHGHRH 536
Db 481 GPVIAKSLTPDNTVGEWQTVFYIAAANVFGAIFFTLFAKGEVQWALNDHHGHRH 536
RESULT 2
US-09-949-016-7705
; Sequence 7705, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7705
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7705
Query Match 98.9%; Score 2804.5; DB 4; Length 585;
Best Local Similarity 95.9%; Pred. No. 2.1e-290;
Matches 534; Conservative 1; Mismatches 1; Indels 21; Gaps 1;
Qy 1 MAAGMT-----PPRPVQAPRGFGGLSGRRSLLCQVASTPAHV 39
Db 29 MAAGSARPLGGTAGTRGRGAVSSPPRPVQAPRGFGGLSGRRSLLCQVASTPAHV 88
Qy 40 GVMSPVRLARNDGEESTDRTLLPGAPRAEAPVCCSARNLAILAFPGFFIYALRV 99
Db 89 GVMSPVRLARNDGEESTDRTLLPGAPRAEAPVCCSARNLAILAFPGFFIYALRV 148
Qy 100 NLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVHNNQTKKYQWDAETQGMILGSFFYG 159
Db 149 NLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVHNNQTKKYQWDAETQGMILGSFFYG 208
Qy 160 YIIQIPGGYVASKIGGKMLLGFILGTAVLTFTPIAADLGVGPLIVLRALEGIGEV 219
Db 209 YIIQIPGGYVASKIGGKMLLGFILGTAVLTFTPIAADLGVGPLIVLRALEGIGEV 268
Qy 220 FPMHAMSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYNNWTVYVFFGTIGI 279
Db 269 FPMHAMSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYNNWTVYVFFGTIGI 328
Qy 280 FFWLLIWLVSDDTPQKHRIISHYEKEYILSSLRNQLSSQKSPVWPILKSLPLWAIIVAH 339
Db 329 FFWLLIWLVSDDTPQKHRIISHYEKEYILSSLRNQLSSQKSPVWPILKSLPLWAIIVAH 388
Qy 340 FSYNWTFTLLTLLPTMKEILRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRKWNF 399
Db 389 FSYNWTFTLLTLLPTMKEILRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRKWNF 448
Qy 400 STL CVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFLLITSTTLGGFCSSGFSINHLDI 459
Db 449 STL CVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFLLITSTTLGGFCSSGFSINHLDI 508

Qy 460 PSYAGILLGTTNTFATIPGMVGPVIAKSLTPDNTVGEWQTVFYIAAANVFGAIFFTLFA 519
Db 509 PSYAGILLGTTNTFATIPGMVGPVIAKSLTPDNTVGEWQTVFYIAAANVFGAIFFTLFA 568
Qy 520 KGEVQWALNDHHGHRH 536
Db 569 KGEVQWALNDHHGHRH 585
RESULT 3
US-09-359-167-2
; Sequence 2, Application US/09359167
; Patent No. 6803448
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/0105
; CURRENT APPLICATION NUMBER: US/09/359,167
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 60-693,843
; EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-359-167-2
Query Match 92.4%; Score 2621; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 6.4e-271;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 42 MRSVPRDLARNDGEESTDRTLLPGAPRAEAPVCCSARNLAILAFPGFFIYALRVNL 101
Db 1 MRSVPRDLARNDGEESTDRTLLPGAPRAEAPVCCSARNLAILAFPGFFIYALRVNL 60
Qy 102 SVALVDMVDSNTTLEDNRTSKACPEHSAPIKVHNNQTKKYQWDAETQGMILGSFFYGYI 161
Db 61 SVALVDMVDSNTTLEDNRTSKACPEHSAPIKVHNNQTKKYQWDAETQGMILGSFFYGYI 120
Qy 162 ITQIPGGYVASKIGGKMLLGFILGTAVLTFTPIAADLGVGPLIVLRALEGIGEV 221
Db 121 ITQIPGGYVASKIGGKMLLGFILGTAVLTFTPIAADLGVGPLIVLRALEGIGEV 180
Qy 222 AMHAMSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYNNWTVYVFFGTIGIFW 281
Db 181 AMHAMSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYNNWTVYVFFGTIGIFW 240
Qy 282 FLLMIWLVSDDTPQKHRIISHYEKEYILSSLRNQLSSQKSPVWPILKSLPLWAIIVAHFS 341
Db 241 FLLMIWLVSDDTPQKHRIISHYEKEYILSSLRNQLSSQKSPVWPILKSLPLWAIIVAHFS 300
Qy 342 YNWTFTLLTLLPTMKEILRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRKWNFST 401
Db 301 YNWTFTLLTLLPTMKEILRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRKWNFST 360
Qy 402 LCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFLLITSTTLGGFCSSGFSINHLDIAPS 461
Db 361 LCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFLLITSTTLGGFCSSGFSINHLDIAPS 420
Qy 462 YAGILLGTTNTFATIPGMVGPVIAKSLTPDNTVGEWQTVFYIAAANVFGAIFFTLFAK 521
Db 421 YAGILLGTTNTFATIPGMVGPVIAKSLTPDNTVGEWQTVFYIAAANVFGAIFFTLFAK 480
Qy 522 EVQWALNDHHGHRH 536
Db 481 EVQWALNDHHGHRH 495
RESULT 4
US-09-915-181A-7

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2005, 05:11:02 ; Search time 116.974 Seconds
(without alignments)
1772.222 Million cell updates/sec

Title: US-09-776-865-2
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqp1990s:*
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4: Geneseqp2001s:*
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6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2836	100.0	536	3 AAY45089	Aay45089 Human GBS
2	2836	100.0	536	4 AAE06518	Aae06518 Human gro
3	2821	92.4	495	3 AAY45087	Aay45087 Partial h
4	2621	92.4	495	4 AAB66967	Aab66967 Human AST
5	2621	92.4	495	8 ADJ75516	Adj75516 Marker ge
6	2621	92.4	495	8 ADR14587	Adr14587 Human NF-
7	2621	92.4	495	8 ADP25217	Adp25217 PRO poly
8	2614	92.2	495	4 AAM38959	Aam38959 Human pol
9	2329	82.1	495	3 AAY45088	Aay45088 Sheep GBS
10	2329	82.1	495	4 AAE06519	Aae06519 Sheep gro
11	1698	59.9	495	3 AAY45090	Aay45090 Human/She
12	1679	59.2	314	4 AAG65238	Aag65238 Human sod
13	1614	56.9	309	4 AAM40745	Aam40745 Human pol
14	1521	53.6	284	5 ABA41345	Abp41345 Human ova
15	1451	51.2	272	5 ABB89975	Abb89975 Human pol
16	1450	51.1	277	4 AAM93314	Aam93314 Human pol
17	1450	51.1	277	8 ADL32036	Adl32036 Human pro
18	996.5	35.1	559	4 ABB58701	Abb58701 Drosophil
19	992	35.0	502	4 ABB65873	Abb65873 Drosophil
20	992	35.0	502	4 ABB60525	Abb60525 Drosophil
21	987	34.8	493	8 ADN23181	Adn23181 Bacterial
22	970	34.2	578	7 ADG88331	Adg88331 Rat trans
23	970	34.2	582	6 ABG74796	Abg74796 Rat DNPI
24	970	34.2	582	6 ABG74797	Abg74797 Murine DN
25	970	34.2	582	6 ABM04787	Abm04787 Rat Na-de

26	970	34.2	582	7 ADC15494	Adc15494 Mouse DNP
27	970	34.2	582	7 ADC15492	Adc15492 Rat DNPI
28	965.5	34.0	582	6 ABG74795	Abg74795 Human DNP
29	965.5	34.0	582	7 ADC15490	Adc15490 Human DNP
30	965.5	34.0	582	7 ADD01475	Add01475 Human VGL
31	959.5	33.8	582	4 AAM79273	Aam79273 Human pro
32	955	33.7	589	5 AAU99329	Aau99329 Human tra
33	955	33.7	589	6 AAO30994	Aao30994 Human tra
34	955	33.7	589	7 ADD01392	Add01392 Human tra
35	955	33.7	589	7 ADG88329	Adg88329 Human tra
36	955	33.7	589	8 ADD10021	Add10021 Human pro
37	945	33.3	601	7 ADD01410	Add01410 Mouse TCH
38	941	33.2	560	6 ABG74791	Abg74791 Human BNP
39	941	33.2	560	7 ADC15482	Adc15482 Human BNP
40	941	33.2	560	7 ADD01474	Add01474 Human VGL
41	941	33.2	567	4 AAO13870	Aao13870 Human pol
42	940.5	33.2	566	7 ADJ95072	Adj95072 Novel NOV
43	940	33.1	560	2 AAW05148	Aaw05148 Human bra
44	940	33.1	560	2 AAW70500	Aaw70500 Human sod
45	940	33.1	560	6 ABG74792	Abg74792 Human BNP

ALIGNMENTS

RESULT 1

AAY45089
ID AAY45089 standard; protein; 536 AA.

XX AAY45089;

XX AC

DT 31-MAY-2000 (first entry)

XX DE Human GBS toxin receptor (HP59).

XX KW Human GBS toxin receptor; group B beta-haemolytic streptococci; HP59;
KW pathological vascularisation; cancer metastases; angiogenesis;
KW neovascularisation; reperfusion injury; scarring; keloid;
KW chronic inflammation; rheumatoid arthritis; psoriasis; neural injury;
KW endothelial cell proliferation; antibacterial; anticancer;
KW anti-angiogenic; anti-inflammatory; anti-arthritis; anti-psoriatic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

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FT Modified-site	23..25	/label= PKC_phospho_site
FT Modified-site	58..60	/note= "Putative phosphorylation site"
FT Modified-site	66..71	/note= "Putative phosphorylation site"
FT Modified-site	78..80	/note= "Putative myristylation site"
FT Modified-site	100..103	/note= "Putative phosphorylation site"
FT Modified-site	112..115	/note= "Asn is N-glycosylated"
FT Modified-site	113..116	/note= "Asn is N-glycosylated"
FT Modified-site	114..117	/note= "Putative phosphorylation site"
FT Modified-site	118..121	/label= CK2_phospho_site
FT Modified-site	120..122	/note= "Putative phosphorylation site"
FT Modified-site	120..122	/note= "Asn is N-glycosylated"
FT Modified-site	120..122	/label= PKC_phospho_site
FT Modified-site	120..122	/note= "Putative phosphorylation site"

FT Modified-site 136. .139 /note= "Asn is N-glycosylated"
 FT Modified-site 138. .141 /note= "Putative amidation site"
 FT Modified-site 138. .140 /label= PKC_phospho_site
 FT Modified-site 167. .172 /note= "Putative phosphorylation site"
 FT Modified-site 183. .188 /note= "Putative myristylation site"
 FT Modified-site 213. .218 /note= "Putative myristylation site"
 FT Modified-site 246. .251 /note= "Putative myristylation site"
 FT Modified-site 250. .255 /note= "Putative myristylation site"
 FT Modified-site 266. .269 /note= "Putative myristylation site"
 FT Modified-site 297. .300 /note= "Asn is N-glycosylated"
 FT Modified-site /label= CAMP_phospho_site
 FT Modified-site 300. .303 /note= "Putative phosphorylation site"
 FT Modified-site /label= CK2_phospho_site
 FT Modified-site 310. .312 /note= "Putative phosphorylation site"
 FT Modified-site /label= PKC_phospho_site
 FT Modified-site 317. .320 /note= "Putative phosphorylation site"
 FT Modified-site /label= PKC_phospho_site
 FT Modified-site 343. .346 /note= "Putative phosphorylation site"
 FT Modified-site /note= "Asn is N-glycosylated"
 FT Modified-site 378. .383 /note= "Putative myristylation site"
 FT Modified-site 398. .401 /note= "Asn is N-glycosylated"
 FT Modified-site 427. .432 /note= "Putative myristylation site"
 FT Modified-site 444. .449 /note= "Putative myristylation site"
 FT Modified-site 464. .469 /note= "Putative myristylation site"
 FT Modified-site 468. .473 /note= "Putative myristylation site"
 FT Modified-site 493. .496 /note= "Putative myristylation site"
 FT Modified-site /label= CK2_phospho_site
 FT Modified-site /note= "Putative phosphorylation site"
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 PN WO200005375-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 22-JUL-1999; 99WO-US016676.
 XX
 PR 22-JUL-1998; 98US-0093843P.
 XX
 PA (UYVA-) UNIV VANDERBILT.
 XX
 PI Hellerqvist CG, Fu C;
 XX
 DR WPI; 2000-205377/18.
 DR N-PSDB; AA250879.
 XX
 PT New polynucleotide encoding mammalian receptor for streptococcus toxin,
 PT useful for diagnosis and treatment of, e.g. pneumonia in neonates.
 XX
 PS Claim 10; Page 93-95; 109pp; English.
 XX
 CC The present sequence is partial human GBS (group B beta-haemolytic
 CC streptococci) toxin receptor (HP5). GBS toxin receptor is an integral
 CC protein with seven transmembrane domains. Expression vectors comprising
 CC the coding region can be transformed into host cells to express GBS toxin

CC receptor and its fragments. Detecting the receptor in tissues is used to
 CC diagnose pathological vascularisation, e.g. for detecting cancer
 CC metastases. GBS toxin receptors are useful for treating conditions
 CC associated with pathological angiogenesis or neovascularisation
 CC (specifically cancer, reperfusion injury, scarring during wound healing,
 CC keloids, chronic inflammation (rheumatoid arthritis or psoriasis) or
 CC neural injury), and to raise specific antibodies used for treating early
 CC onset disease. Inhibitors of this receptor are useful for treating
 CC pathological or hypoxia-induced endothelial cell proliferation and
 CC migration
 XX
 SQ Sequence 536 AA;
 Query Match 100.0%; Score 2836; DB 3; Length 536;
 Best Local Similarity 100.0%; Pred. No. 1.5e-282;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAAGAMTPPRPVQPARPGFGLSGRRSLLCQVASTPAHVGMRSVPVRLDARNDGEESTDR 60
 Db 1 MAAGAMTPPRPVQPARPGFGLSGRRSLLCQVASTPAHVGMRSVPVRLDARNDGEESTDR 60
 Qy 61 TPLLPGAPRAEAPVCCSARYNLAILAFGGFFIVYALRVNLVALVDMVDSNTTLENDRT 120
 Db 61 TPLLPGAPRAEAPVCCSARYNLAILAFGGFFIVYALRVNLVALVDMVDSNTTLENDRT 120
 Qy 121 SKACPEHSAPIKVHHNQTGKKYQWDAETQGWILGSPFYGYIITQIPGGYVASKIGKML 180
 Db 121 SKACPEHSAPIKVHHNQTGKKYQWDAETQGWILGSPFYGYIITQIPGGYVASKIGKML 180
 Qy 181 GFGILGTAVLTFTPIAADLGVGLIVLRALEGLGEGVTFPAMHAMSSWAPPLERSKLL 240
 Db 181 GFGILGTAVLTFTPIAADLGVGLIVLRALEGLGEGVTFPAMHAMSSWAPPLERSKLL 240
 Qy 241 SISYAGAQLGTVISLPLSGIICYYMNTVYVYFFGTIGIFWLLIWLVS DTPQKHRS 300
 Db 241 SISYAGAQLGTVISLPLSGIICYYMNTVYVYFFGTIGIFWLLIWLVS DTPQKHRS 300
 Qy 301 HYEKEYILSLRNQLSSQKSPVWPVPLKSLPLMAIVVAHFSYNWTFYTLTLTLLPTMKEI 360
 Db 301 HYEKEYILSLRNQLSSQKSPVWPVPLKSLPLMAIVVAHFSYNWTFYTLTLTLLPTMKEI 360
 Qy 361 LRFNVQENGFLSSLPYLGSLWLCMILSQQAADNLRAKNFSTLCVRRIFSLIGMIGPAVL 420
 Db 361 LRFNVQENGFLSSLPYLGSLWLCMILSQQAADNLRAKNFSTLCVRRIFSLIGMIGPAVL 420
 Qy 421 VAAGFIGCDYSLAVAFITITLGGFCSSGFSINHLDIAPSYAGILIGITNTFATIGMV 480
 Db 421 VAAGFIGCDYSLAVAFITITLGGFCSSGFSINHLDIAPSYAGILIGITNTFATIGMV 480
 Qy 481 GPVIAKSLTPDNTVGEWQTVFYIAAAINVFGAIFFTLFAKGEVQNWALNDHHGHRH 536
 Db 481 GPVIAKSLTPDNTVGEWQTVFYIAAAINVFGAIFFTLFAKGEVQNWALNDHHGHRH 536
 RESULT 2
 AAE06518
 ID AAE06518 standard; protein; 536 AA.
 XX
 AC AAE06518;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human group B beta-haemolytic Streptococci toxin receptor (HP59) protein.
 XX
 KW Human; group B beta-haemolytic Streptococci toxin receptor; GBS; HP59;
 KW cytosolic; vulnery; antiatherosclerotic; osteopathic; vasotropic;
 KW prevention; attenuation; pathoangiogenic condition; cancer; scar;
 KW wound healing; gliosis; nerve injury; chronic wound; reperfusion injury;
 KW keloid; rheumatoid arthritis; atherosclerosis; osteoarthritis; psoriasis;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX